

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 07:10:31 ; Search time 1927 Seconds  
(without alignments)  
15833.363 Million cell updates/sec

Title: US-09-918-359-6

Perfect score: 1458  
Sequence: 1 atgagctcagcctcgtgga.....acctgtgctgtgaggtga 1458

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sta:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_of:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sta:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hcgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

1	915	62.8	4695	9	HSMB02204	AL137479 Homo sapi
2	324.2	22.2	2200	9	AK023366	AK023366 Homo sapi
3	243.8	16.7	14724	2	AP003779	AP003779 Homo sapi
4	243.8	16.7	186974	2	AP003071	AP003071 Homo sapi
5	243.8	16.7	194781	2	AC019124	AC019124 Homo sapi
6	242	16.6	381	6	AX071636	AX071636 Sequence
7	157.8	10.8	520	11	G72237	G72237 Stn17 Stick
8	137.8	9.5	194781	2	AC019124	AC019124 Homo sapi
9	79.2	5.4	162797	2	AC098981	AC098981 Rattus no
10	75.4	5.2	162797	2	AC098981	AC098981 Rattus no
11	68.4	4.7	70673	2	AC091258	AC091258 Mus muscu
12	67.2	4.6	2742	10	AF217002	AF217002 Mus muscu
13	62.4	4.3	4743	10	AB018253	AB018253 Rattus no
14	60	4.1	1608	6	AX068907	AX068907 Sequence
15	60	4.1	7044	9	HSAB20779	HSAB20779 Homo sapi
16	60	4.1	7762	9	AF051946	AF051946 Homo sapi
17	60	4.1	7898	9	AF073931	AF073931 Homo sapi
18	59.8	4.1	2448	6	AX235890	AX235890 Sequence
19	59.8	4.1	2858	9	AK057414	AK057414 Homo sapi
20	59.8	4.1	4023	6	AX061213	AX061213 Sequence
21	59.8	4.1	4836	9	AB032995	AB032995 Homo sapi
22	59.8	4.1	5269	6	AX235888	AX235888 Sequence
23	57.6	4.0	125020	9	AF429315	AF429315 Homo sapi
24	57	3.9	2870	3	AF029249	AF029249 Mytilus e
25	55.8	3.8	125020	9	AF429315	AF429315 Homo sapi
26	53.6	3.7	6160	9	HUMCACNTA	U37398 Human d1hyd
27	52.4	3.6	885	9	HUMTR2R3	D15055 Homo sapien
28	52.4	3.6	1277	9	AF017452	AF017452 Cercopith
29	52.4	3.6	1492	9	HSU11271	U11271 Human alter
30	52.4	3.6	2932	6	E03829	E03829 CDNA encodi
31	52.4	3.6	2932	6	HUMHTRAR	D38081 Human mRNA
32	52.4	3.6	41303	9	AC005175	AC005175 Homo sapi
33	52.4	3.6	175625	2	AC068475	AC068475 Homo sapi
34	52.4	3.6	250227	2	AC093363	AC093363 Mus muscu
35	52.2	3.6	16013	9	AP001648	AP001648 Homo sapi
36	51.8	3.6	158063	9	AP001046	AP001046 Homo sapi
37	51.8	3.6	340000	9	AP001751	AP001751 Homo sapi
38	51.6	3.5	88203	5	AC097628	AC097628 Takifugu
39	51.2	3.5	203691	2	AC098980	AC098980 Rattus no
40	50.8	3.5	1323	9	HSU27325	U27325 Human throm
41	50.8	3.5	6010	10	MUSCACHB	L06234 Mus musculu
42	50.6	3.5	5975	6	I09517	I09517 Sequence 1
43	50.6	3.5	5975	6	I40161	I40161 Sequence 1
44	50.6	3.5	5975	6	I73184	I73184 Sequence 1
45	50.6	3.5	5975	6	I81460	I81460 Sequence 1

## ALIGNMENTS

RESULT 1  
LOCUS HSM802204  
DEFINITION Homo sapiens mRNA; cDNA DKFp434M0223 (from clone DKFp434M0223); partial cds.  
ACCESSION AL137479  
VERSION AL137479.1 GI:6808092  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 4695)  
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; Munich/Germany) within the CDNA sequencing consortium of the German Genome Project.  
This clone (DKFp434M0223) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY. Email: clone@rzd.de. Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cdna/>.

## FEATURES

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/db\_xref="taxon:9606"  
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/tissue\_type="testis"  
/clone\_id="434 (synonym: hies3). Vector pSport1; host DH10B; sites NotI + SalI"  
/dev\_stage="adult"  
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1. 1118  
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/product="hypothetical protein"  
/protein\_id="CAI70760.1"  
/db\_xref="GI:6808093"  
/translation="KVRYSYVLSAEPOKLFNEDRSVKEHPREYOSPFLOSA  
OFLFGHYEDYGLNIALANVSIQVFLVDADVFAERDDFLGLNCFVIVYLLLE  
MLKVFALGRLGYSNPVDFGLVFLVLEISLAVRILPHPMREMGILSLM  
DMRMLNMLIVREFRLIIPSMKPMAYASTAVIGVONMAFGIIVVVYVEVILGIN  
LFRGVIVAPGNSIAPANGSAPCGSPDELEFMANDEPAALVATLNMVNMNOY  
FLDAYRHSFPMKSTIFVLMVLISSYIVNVLALLENFLHKNDRSHLOPLAGIPE  
ATVOMTELLFELDFEPEDELTERLSOHPHMLDCK"

gene  
CDS  
polyA\_signal  
polyA\_site  
BASE COUNT 1141 a 1144 c 1249 g 1161 t

Query Match 62.8%; Score 915; DB 9; Length 4695;  
Best Local Similarity 94.7%; Pred. No. 7.7e-182;  
Matches 978; Conservative 0; Mismatches 5; Indels 50; Gaps 1;

476 AGGCCACCGCCGCGGACGATGCTCCGTTCTGACAGAGCCGACGATCTCTT 535  
86 AGAGACCGCCGCGGACGATGCTCCGTTCTGACAGAGCCGACGATCTCTT 145  
536 CGGCCACTACTACTTTGACTACCTGGGAACTCATGCGCTGGCAAACTGTGTCCAT 595  
146 CGGCCACTACTACTTTGACTACCTGGGAACTCATGCGCTGGCAAACTGTGTCCAT 205  
596 TTGCGTGTCTGCTGCTGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655  
206 TTGCGTGTCTGCTGCTGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265  
596 GGGGATCTCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715  
266 GGGGATCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325  
716 TGCCCTGGGCTGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775  
326 TGCCCTGGGCTGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385  
776 CGTTGCTCT-----G 785  
386 CGTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445  
786 CTGAGAGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845  
446 CTGAGAGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 505  
846 GCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905  
506 GCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 565  
906 CAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965

Db 566 CAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625  
Qy 966 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1025  
Db 626 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 685  
Qy 1026 TGGAACAGCAGCCTGCGCCCTGCAATGCTGCGCCCTGCTGCGAGCTTGCAGCAGCT 1085  
Db 686 TGGAACAGCAGCCTGCGCCCTGCAATGCTGCGCCCTGCTGCGAGCTTGCAGCAGCT 745  
Qy 1086 GAGTACTGCGCCCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1145  
Db 746 GAGTACTGCGCCCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 805  
Qy 1146 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205  
Db 806 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 865  
Qy 1206 GTCCAGATCTATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1265  
Db 866 GTCCAGATCTATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925  
Qy 1266 TCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325  
Db 926 TCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 985  
Qy 1326 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385  
Db 986 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045  
Qy 1386 TCTGAGAGAGCCCGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445  
Db 1046 TCTGAGAGAGCCCGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105  
Qy 1446 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1458  
Db 1106 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118

RESULT 2  
AK023366  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
1 (sites)  
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,  
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,  
Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,  
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,  
Oho, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakawa, K.,  
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,  
Nakamura, Y., Nagahara, K., Masuho, Y., Minomiyama, K. and Iwayanagi, T.  
NEDO human cDNA sequencing project  
Unpublished (2000)

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Isogai, T. and Otsuki, T.  
Direct Submission  
Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao  
Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana,  
Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp,  
Tel: 81-438-52-3951, Fax: 81-438-52-3952)

COMMENT  
NEDO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan: cDNA full insert  
sequencing: Research Association for Biotechnology: cDNA library  
construction, 5'- & 3'-end one pass sequencing and clone selection:  
Helix Research Institute (supported by Japan Key Technology Center







```

159380      162427 contig of 3048 bp in length
165228      165945 contig of 3418 bp in length
166046      168780 contig of 2735 bp in length
169800      169300 contig of 420 bp in length
169404      171169 contig of 1769 bp in length
171270      172788 contig of 1519 bp in length
172869      174327 contig of 1439 bp in length
174428      176380 contig of 1953 bp in length
176481      178019 contig of 1539 bp in length
178120      179796 contig of 1677 bp in length
179897      182113 contig of 2217 bp in length
182214      182331 contig of 138 bp in length
182452      184413 contig of 1962 bp in length
184514      185839 contig of 1326 bp in length
185440      186974 contig of 1035 bp in length

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1	19869	contig of	19869	bp	in	length
*	19870	19869: gap of	100	bp		
*	19870	39911: contig of	19942	bp	in	length
*	39912	40011: gap of	100	bp		
*	40012	56821: contig of	16810	bp	in	length
*	56822	56921: gap of	100	bp		
*	56922	70687: contig of	13766	bp	in	length
*	70688	70787: gap of	100	bp		
*	70788	85173: contig of	14386	bp	in	length
*	85174	85223: gap of	100	bp		
*	85274	95216: contig of	9943	bp	in	length
*	95217	95316: gap of	100	bp		
*	95317	106242: contig of	10926	bp	in	length
*	106243	106342: gap of	100	bp		
*	106343	115022: contig of	8680	bp	in	length
*	115023	115122: gap of	100	bp		
*	115123	120641: contig of	5519	bp	in	length
*	120642	120741: gap of	100	bp		
*	120742	127870: contig of	7129	bp	in	length
*	127871	127970: gap of	100	bp		
*	127971	133204: contig of	5234	bp	in	length
*	133205	133304: gap of	100	bp		
*	133305	138309: contig of	5005	bp	in	length
*	138310	138409: gap of	100	bp		
*	138410	143433: contig of	5024	bp	in	length
*	143433	143533: gap of	100	bp		
*	143534	149691: contig of	6158	bp	in	length
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*	159280	159379: gap of	100	bp		
*	159380	162427: contig of	3048	bp	in	length
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*	162528	165945: contig of	3418	bp	in	length
*	165946	166045: gap of	100	bp		
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*	169401	171169: contig of	1769	bp	in	length
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*	171270	172786: contig of	1519	bp	in	length
*	172789	172888: gap of	100	bp		
*	172890	174327: contig of	1439	bp	in	length
*	174328	174427: gap of	100	bp		
*	174428	176380: contig of	1953	bp	in	length
*	176381	176480: gap of	100	bp		
*	176481	178019: contig of	1539	bp	in	length
*	178020	178119: gap of	100	bp		

FEATURES	Source
*	178120 179796: contig of 1677 bp in length
*	179797 179896: gap of 100 bp
*	179897 182113: contig of 2217 bp in length
*	182114 182213: gap of 100 bp
*	182214 182351: contig of 138 bp in length
*	182352 182451: gap of 100 bp
*	182452 184413: contig of 1962 bp in length
*	184414 184513: gap of 100 bp
*	184514 185839: contig of 1326 bp in length
*	185840 185939: gap of 100 bp
*	185940 186974: contig of 1035 bp in length.
	Location/Qualifiers
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/chromosome="11"
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56922..70687
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171270..172788
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Query Match	16.7%;	Score 243.8;	DB 2;	Length 186974;
Best Local Similarity	99.2%;	Pred. No. 5.9e-41;		
Matches 245;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0;

QY 1 ATGAGCTAGCCTCTGGGAGAGCCACACAGGAGATGACAGCCTGGGCGCGGGGTGGATGGTT 60  
QY DB 141339 ATGAGCTAGCCTCTGGGAGAGCCACACAGGAGATGACAGCCTGGGCGCGGGGTGGATGGTT 141398  
QY 61 CCAACCGTTGGGATCCGGGCGCTGGAGCTGAGCTGAGGGGTGGGAGCCACAGTGGTGGCC 120

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Db 141399 CCAAGCCGGTGGGTCGGGGCCCTGGAGCTGAGCTGTGGGGTGGGAGCCCAAGTGTGCC 141458
QY 121 TGGAGCTGCGCTTCTGCTCTCAGCAGATGATGAGCAGAGGAGAGCTGACCTAC 180
Db 141459 TGGAGCTGCGCTTCTGCTCTTTCAGAGATGATGAGCAGAGGAGAGGCTGACCTAC 141518
QY 181 TTCAGAACCTGCTGAGTCTGACTTCCCTCTGCTGCTGACCAAGGCGCAAC 240
Db 141519 TTCAGAACCTGCTGAGTCTGACTTCCCTCTGCTGCTGACCAAGGCGCAAC 141578
QY 241 CCGGATG 247
Db 141579 CCGGATG 141585

RESULT 5
AC019124/c
LOCUS AC019124 194781 bp DNA linear HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-554A11, WORKING DRAFT
ACCESSION AC019124
VERSION AC019124.4 GI:8568923
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 194781)
AUTHORS Waterston R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 194781)
TITLE Waterston, R.H.
JOURNAL Direct Submission
COMMENT Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7408149.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0554A11
----- Summary Statistics -----
Sequencing vector: pLasmid: 128
Chemistry: Dye-Primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 174246 bases at least Q40
Consensus quality: 180170 bases at least Q30
Consensus quality: 183510 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 192181; sum-of-ctrls
Quality coverage: 3.73 in Q20 bases; agarose-fp
Quality coverage: 3.93 in Q20 bases; sum-of-ctrls
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1121: contig of 1121 bp in length
* 1122 1221: gap of unknown length
* 1222 2371: contig of 1150 bp in length
* 2372 2472: gap of unknown length
* 2472 4256: contig of 1785 bp in length
* 4256 4357: gap of unknown length

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* 4357 6564: contig of 2208 bp in length
* 6565 9101: gap of unknown length
* 9101 9201: contig of 2437 bp in length
* 9201 9202: gap of unknown length
* 9202 12243: contig of 3041 bp in length
* 12243 12343: gap of unknown length
* 12343 15317: contig of 2974 bp in length
* 15317 15417: gap of unknown length
* 15417 18828: contig of 3412 bp in length
* 18828 18928: gap of unknown length
* 18928 22949: contig of 4021 bp in length
* 22949 23050: gap of unknown length
* 23050 25848: contig of 2799 bp in length
* 25848 25949: gap of unknown length
* 25949 30458: contig of 4509 bp in length
* 30458 30558: gap of unknown length
* 30558 35981: contig of 5423 bp in length
* 35981 36081: gap of unknown length
* 36081 41245: contig of 5165 bp in length
* 41245 41345: gap of unknown length
* 41345 47770: contig of 6425 bp in length
* 47770 47871: gap of unknown length
* 47871 54231: contig of 6360 bp in length
* 54231 54331: gap of unknown length
* 54331 63805: contig of 9475 bp in length
* 63805 63905: gap of unknown length
* 63905 72873: contig of 8967 bp in length
* 72873 72972: gap of unknown length
* 72972 81072: gap of 8100 bp in length
* 81072 81172: contig of 10270 bp in length
* 81172 91442: gap of unknown length
* 91442 91543: gap of 9619 bp in length
* 91543 101162: gap of unknown length
* 101162 101261: gap of 11572 bp in length
* 101261 112833: contig of 13199 bp in length
* 112833 112933: gap of unknown length
* 112933 126132: contig of 11711 bp in length
* 126132 126232: gap of unknown length
* 126232 137943: contig of 13541 bp in length
* 137943 138043: gap of unknown length
* 138043 151584: gap of 13564 bp in length
* 151584 151685: gap of unknown length
* 151685 165049: contig of 13564 bp in length
* 165049 178773: gap of unknown length
* 178773 178874: contig of 13625 bp in length
* 178874 194781: gap of unknown length
* 194781 194781: contig of 15908 bp in length.

FEATURES
source
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/db_xref="taxon:9606"
/chromosome="11"
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/note="assembly_name:Contig6"
1222..2371
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6665..9101
/note="assembly_name:Contig10"
9202..12243
/note="assembly_name:Contig11"
12343..15316
/note="assembly_name:Contig12"
15417..18828
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18929..22949
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23050..25848
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misc_feature	30558. .35980	/note="assembly_name:Contig17"
misc_feature	36081. .41245	/note="assembly_name:Contig18"
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misc_feature	63906. .72872	/note="assembly_name:Contig22"
misc_feature	72973. .81072	/note="assembly_name:Contig23"
misc_feature	81173. .91442	/note="assembly_name:Contig24"
misc_feature	91543. .101161	/note="assembly_name:Contig25"
misc_feature	101262. .112853	/note="assembly_name:Contig26"
misc_feature	112934. .126132	/note="assembly_name:Contig27"
misc_feature	126233. .137943	/note="assembly_name:Contig28"
misc_feature	138044. .151584	/note="assembly_name:Contig29"
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misc_feature	165149. .178773	/note="assembly_name:Contig31"
misc_feature	178874. .194781	/note="assembly_name:Contig32"

BASE COUNT	a	c	g	t	others
ORIGIN	45508	50858	51838	43921	2656

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Best Local Similarity	99.2%;	Pred. NO. 5.9e-41;		
Matches 245; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	ATGAGCTCAGCCTCTGTGGAGAGCCACAGAGGAGATGCAAGGCTGGGGCGGGGTGGATGGTT	60
Db	148271	ATGAGCTCAGCCTCTGTGGAGAGCCACAGGAGATGCAAGGCTGGGGCGGGGTGGATGGTT	148212
QY	61	CCACACCGGTTGGGTGCCGGGGCTTGGAGCTCAGCCTGTGGGGTGGGGACCCAGTGTGCC	120
Db	148211	CCAGCGGGTTGGGTGCCGGGGCTTGGAGCTCAGCCTGTGGGGTGGGGACCCAGTGTGCC	148152
QY	121	TGGAGCTCCGCTTCTGTGCTCAGCAGGATATGAGGACAGACAGGAGAGGCTAGCTTAC	180
Db	148151	TGGAGCTCCGCTTCTGTGCTTTCACAGGATATGAGGACAGACAGGAGAGGCTAGCTTAC	148092
QY	181	TTTCAGAACCTGCCTGAGTCTCTGACTTCCCTCCTGGTGTGCTGACACAGGCCAACAC	240
Db	148091	TTTCAGAACCTGCCTGAGTCTCTGACTTCCCTCCTGGTGTGCTGACACAGGCCAACAC	148032
QY	241	CCCCGATG 247	
Db	148031	CCCCGATG 148025	

RESULT	6
AX071636	
LOCUS	381 bp DNA
DEFINITION	Ax071636 Sequence 2108 from Patent WO0102568.
ACCESSION	AX071636
VERSION	AX071636.1 GI:12581987
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens
PAT	25-JAN-2001
linear	

REFERENCE	Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 381) Williams, J.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Poc, D., Lamsan, G., Dimanac, R., Cirenjakov, R., Dimanac, S., Dickson, M., Labat, I., Ieshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.		
TITLE	Human genes and gene expression products		
JOURNAL	Patent: WO 0102568-A 2108 11-JAN-2001;		
FEATURES	CHIRON CORPORATION (US) ; HYSQO, INC. (US)		
SOURCE	Location/Qualifiers 1..381 /organism="Homo sapiens" /db_xref="taxon:9606"		
BASE COUNT	75 a	121 c	94 g 91 t
ORIGIN			

Query Match	16.6%;	Score 242;	DB 6;	Length 381;
Best Local Similarity	76.4%;	Pred. No. 1.2e-40;		
Matches 359;	Conservative 0;	Mismatches 10;	Indels 101;	Gaps 1

QY	136	TGTCCTGACGAGGATGATGGGACAGACACGAGGAGAGGCTACCTTCTCCAAACCTGGCT	194
Db	4	TGCTCTCGGCGAGGATGATGGGACAGACACGAGGAGAGGCTACCTTCTCCAAACCTGGCT	63
QY	196	GAGTCTCGACTTCCCTCTGCTGCTGTGACCCACGCGCCAAACCCCGATGTGATTT	255
Db	64	GAGTCTCGACTTCCCTCTGCTGCTGTGATGACCAAGCGCCAAACCCCGATGTGATTT	121
QY	256	CCTGGTATTCACAAACCGGGCCATATGCATCTCTTCAATAGTTTACAGTGTATAGA	311
Db	124	CCTGGTATTCACAAACCGGGCCATATGCATCTTCTCATAGCTTACATGTATAGA	181
QY	316	AGCCTGTTTCTGATGAACCTGCTGACACAGCATCATCTACAGTCAAGTTCCGGGGCTACCTG	371
Db	184	AGCCTGTTTCTGATGAACCTGCTGACACAGCATCATCTACAGTCAAGTTCCGGGGCTACCTG	241
QY	376	ATGAATCTCTTCACACCTCGCTGTTTGGGAGGGCGGTGGAAACCCGGGGCTGCTTGA	431

Db	244	ATG-----	246
Qy	436	GTCCATTCCTCCATG6TGGGGAG6AGAGCCTCCCGACAGCCACCGCCGAGGCCG	495
Db	247	-----CACCCGCCGAGGCCCG	262
Qy	496	AGTACAGTCTCGTTTCGACAGACGCCACTTCCTCTCGGCCACTACTACTTTGACT	555
Db	263	ACTACAGACTCGTTTCTGCGACAGCCCACTTCCTCTTGCGCCACTACTACTTTGACT	322
Qy	556	ACCTGGGGAACCTCATCGCCCTGGCAAACTGGTGCATTTGGCGTGTTC	605
Db	323	ACCTGGGGAACCTTATCGACCTGGCAAACTGGTGCATTTGGCGATTC	372

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
G72237	520 bp	Stu1f Stickleback cDNA Gasterosteus aculeatus STS clone	G72237			GI:17977097	three spined stickleback.			
G72237	mRNA	linear STS 21-DEC-2001	G72237				Gasterosteus aculeatus			
		65-32/73, sequence tagged site.					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
							Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
							Acanthomorpha; Acanthopterygii; Percormorpha; Gasterosteiformes;			
							Gasterosteidae; Gasterosteus.			
							1 (bases 1 to 520)			
							Pelichel,C.L., Nereyng,K.S., Ohgi,K.A., Cole,B.L., Colosimo,P.F.,			
							Buerkle,C.A., Schluter,D. and Kingsley,D.M.			
							The genetic architecture of divergence between threespine			
							stickleback species			

JOURNAL Nature 414 (6866), 901-905 (2001)  
 PUBMED 11780061  
 COMMENT Synonyms: A10yellow11

Contact: David M. Kingsley  
 Dept of Developmental Biology/ Howard Hughes Medical Institute  
 Stanford University School of Medicine  
 3800 Beckman Center, 279 Campus Drive, Stanford, CA 94305-5329, USA  
 Email: kingsley@cmmg.stanford.edu  
 Primer A: AGAGAGCAGATCCAGAGACC  
 Primer B: GCATTCACCTGACCTCCAGG  
 STS size: 145

PCR Profile:  
 Denaturation: 95 degrees C for 1:45  
 Annealing: 56 degrees C for 0:45  
 Polymerization: 72 degrees C for 0:45  
 PCR cycles: 1  
 Denaturation: 94 degrees C for 0:45  
 Annealing: 56 degrees C for 0:45  
 Polymerization: 72 degrees C for 0:45  
 PCR cycles: 4  
 Denaturation: 90 degrees C for 0:45  
 Annealing: 56 degrees C for 0:45  
 Polymerization: 72 degrees C for 0:45  
 PCR cycles: 30  
 Thermal cycler: MJ Research PTC-200 DNA Engine

Protocol:  
 Template: 5 ng  
 Primer: each 0.5 uM  
 dNTPs: each 62.5 uM  
 Taq polymerase: 0.25 units  
 Total volume: 10 uL

Buffer:  
 MgCl2: 1.5 mM  
 KCl: 50 mM  
 Tris-HCl: 10 mM  
 pH: 8.3  
 Location/Qualifiers  
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 /strain="Salinas River, California"  
 /db\_xref="taxon:69293"  
 /clone="65-32/73"  
 /tissue\_type="head and internal organs"  
 /clone\_11b="Stickleback cDNA"  
 /dev\_stage="Adult"  
 /lab\_host="XLI-Blue MRF"  
 /note="Vector: ZAP Express; V-type: Phage: Oligo(dT)  
 primed cDNA unidirectionally cloned into the EcoRI/XhoI  
 sites of ZAP Express."

STs  
 primer\_bind 329..473  
 primer\_bind 329..348  
 BASE COUNT 131 a 129 c 131 g 125 t 4 others  
 ORIGIN

Query Match 10.8%; Score 157.8; DB 11; Length 520;  
 Best Local Similarity 64.4%; Pred. No. 5.6e-23;  
 Matches 253; Conservative 0; Mismatches 137; Indels 3; Gaps 1;

QY 1066 TGTGGAGAGCTTGAGCAGCTGAGGAGCACTTGAGTACCTTTGGGCTGCGC 1125  
 DB 20 TGTGGAGAGCTTGAGCAGCTGAGGAGCACTTGAGTACCTTTGGGCTGCGC 79  
 QY 1126 CTGTGACCTCTGTGAACTGTGAGTGTGAACTGAGTGTGCTGTGATGAT 1185  
 DB 80 ATCATCTTCTGTACACACTGATGCTGTGATGATGAGGCTTCTGTGATGAT 139  
 QY 1186 CGGCGTACTCAGGCGCTGTGCAAGATCTATTTGTATTTGTGTGCTGTGCT 1245  
 DB 140 ACCCGCACACACACATGATGCTGTGCAAGATCTATTTGTGTGCTGTGCT 199  
 QY 1246 GTCATCTGTGAGTACCTGTTTGTGCGCTGTGAGTGTGAGTCTCTTCAACAAGTGGAC 1305

DB 200 GTCATCTGTGAGTACCTGTTTGTGCTGTGAGTGTGAGTCTCTTCAACAAGTGGAC 258  
 QY 1306 CCCCCAGCACCTGTCAGAGCCCTTGTGAGACCCAGACCCACCTACAGATGCTGTG 1365  
 DB 259 -CCGTAGTCAACAGCTCTCTGTGATGATGAGAGATCCGATATGAAACATCTGT 316  
 QY 1366 GAGCTCTGTGAGATATTTGTGAGAGCCCGGAGAGATGAGCTCACAGAGAGCTG 1425  
 DB 317 CAGTCTATTTACAGAGCAGATCCAGAGCCAGCCAGAGGATTAATCTGTCTACTTA 376  
 QY 1426 AGCCAGCAGCCGACCTGTGCTGTGAGTGA 1458  
 DB 377 AACCTCACCCCACTTACACCTACACTGTGA 409

RESULT 8  
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 LOCUS  
 DEFINITION  
 Homo sapiens chromosome 11 clone RP11-554A11, WORKING DRAFT  
 AC019124  
 VERSION  
 AC019124.4 GI:8568923  
 KEYWORDS  
 HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 194781)  
 Waterston, R.H.  
 The sequence of Homo sapiens clone  
 2 (bases 1 to 194781)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (30-DEC-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Jun 16, 2000 this sequence version replaced gi:7408149.

Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 Project Information  
 Center project name: H.NH0554A11  
 Summary Statistics  
 Sequencing vector: p13; 888  
 Sequencing vector: plasmid; 128  
 Chemistry: Dye-terminator ET; 88% of reads  
 Chemistry: Dye-terminator Big Dye; 12% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 174246 bases at least Q40  
 Consensus quality: 180170 bases at least Q30  
 Consensus quality: 183510 bases at least Q20  
 Insert size: 197000; agarose-fp  
 Insert size: 192181; sum-of-coverage  
 Quality coverage: 3.73 in Q20 bases; agarose-fp  
 Quality coverage: 3.93 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently  
 consists of 27 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1  
 1121: contig of 1121 bp in length  
 1122: gap of unknown length  
 1222: contig of 1150 bp in length  
 2372: gap of unknown length  
 2472: contig of 1785 bp in length



REFERENCE  
AUTHORS

Ratus.  
1 (bases 1 to 162797)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amaralunge,H.C., Are,U.R., Banks,T., Barbata,J.,  
Benton,J., Bimaga,M., Blankenburg,K., Bonin,D., Bouck,J.,  
Bowle,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P., Buhaq,C.,  
Burck,P., Burckell,C., Burrell,K.L., Byrd,N.C., Carton,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,  
Coyte,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Dean,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,  
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Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,  
Garcia,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S.,  
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,  
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,  
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Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,U., Liu,M.,  
Louisege,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,  
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,  
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,  
Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,  
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,  
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,  
Ogulu,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,  
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojokan,I., Rolfe,L.,  
Ruliz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shochter,I.,  
Stinson,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H.,  
Stone,H., Sutton,A., Swatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,  
Tang,H., Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N.,  
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,  
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,  
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,  
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

Direct Submission  
Unpublished  
2 (bases 1 to 162797)  
Worley,K.C.

Submitted (08-NOV-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Dec 21, 2001 this sequence version replaced gi:17062421.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GGNZ  
Center clone name: CH230-112J19  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329first call to  
findhapluplist  
Consensus quality: 121859 bases at least Q40  
Consensus quality: 132629 bases at least Q30  
Consensus quality: 141983 bases at least Q20  
Estimated insert size: 130105; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-gel estimation  
Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 73 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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12193	12292:	gap of unknown	length
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16879	16978:	gap of unknown	length
16979	22042:	contig of 5064	bp in length
22043	22142:	gap of unknown	length
22143	26328:	contig of 4186	bp in length
26329	26428:	gap of unknown	length
26429	30885:	contig of 4457	bp in length
30886	30985:	gap of unknown	length
30986	35472:	contig of 4487	bp in length
35473	35572:	gap of unknown	length
35573	38723:	contig of 3151	bp in length
38724	38823:	gap of unknown	length
38824	41201:	contig of 2378	bp in length
41202	41301:	gap of unknown	length
41302	44535:	contig of 3238	bp in length
44536	44639:	gap of unknown	length
44640	46877:	contig of 2238	bp in length
46878	46977:	gap of unknown	length
46978	49434:	contig of 2457	bp in length
49435	49534:	gap of unknown	length
49535	52560:	contig of 3026	bp in length
52561	52660:	gap of unknown	length
52661	55663:	contig of 3003	bp in length
55664	55663:	gap of unknown	length
55664	59736:	contig of 3073	bp in length
59737	59836:	gap of unknown	length
59837	62599:	contig of 2763	bp in length
62600	62699:	gap of unknown	length
62700	65378:	contig of 2679	bp in length
65379	65478:	gap of unknown	length
65479	67635:	contig of 2157	bp in length
67636	67735:	gap of unknown	length
67736	69998:	contig of 2263	bp in length
69999	70098:	gap of unknown	length
70099	71794:	contig of 1696	bp in length
71795	71894:	gap of unknown	length
71895	74075:	contig of 2181	bp in length
74076	74175:	gap of unknown	length
74176	75899:	contig of 1724	bp in length
75900	75999:	gap of unknown	length
76000	77326:	contig of 1327	bp in length
77327	77426:	gap of unknown	length
77427	79222:	contig of 1796	bp in length
79223	79322:	gap of unknown	length
79323	81657:	contig of 2335	bp in length
81658	81757:	gap of unknown	length
81758	84091:	contig of 2334	bp in length
84092	84191:	gap of unknown	length
84192	86275:	contig of 2084	bp in length
86276	86375:	gap of unknown	length
86376	88039:	contig of 1664	bp in length
88040	88139:	gap of unknown	length
88140	90082:	contig of 1943	bp in length
90083	90182:	gap of unknown	length
90183	92332:	contig of 2150	bp in length
92333	92432:	gap of unknown	length
92433	94341:	contig of 1909	bp in length
94342	94441:	gap of unknown	length
94442	96459:	contig of 2018	bp in length
96460	96559:	gap of unknown	length
96560	97677:	contig of 1118	bp in length
97678	97777:	gap of unknown	length
97778	100571:	contig of 2794	bp in length
100572	100671:	gap of unknown	length

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* 10672 103294: contig of 2623 bp in length
* 103295 103947: gap of unknown length
* 103395 105407: contig of 2013 bp in length
* 105408 105507: gap of unknown length
* 105508 107416: contig of 1909 bp in length
* 107417 107516: gap of unknown length
* 107517 109199: contig of 1683 bp in length
* 109200 109299: gap of unknown length
* 109300 110432: contig of 1133 bp in length
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* 110533 111730: contig of 1198 bp in length
* 111731 111830: gap of unknown length
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* 113304 115014: contig of 1711 bp in length
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* 115115 115267: contig of 1153 bp in length
* 115268 116367: gap of unknown length
* 116368 117721: contig of 1354 bp in length
* 117722 117821: gap of unknown length
* 117822 120156: contig of 2335 bp in length
* 120157 120256: gap of unknown length
* 120257 122253: contig of 1997 bp in length
* 122254 122353: gap of unknown length
* 122354 123767: contig of 1414 bp in length
* 123768 123867: gap of unknown length
* 123868 125213: contig of 1346 bp in length
* 125214 125313: gap of unknown length
* 125314 126628: contig of 1315 bp in length
* 126629 126728: gap of unknown length
* 126729 128396: contig of 1668 bp in length
* 128397 128497: gap of unknown length
* 130420 130420: contig of 1924 bp in length
* 130421 130520: gap of unknown length
* 130521 132161: contig of 1641 bp in length
* 132162 132261: gap of unknown length
* 132262 133666: contig of 1405 bp in length
* 133667 133766: gap of unknown length
* 133767 135414: contig of 1648 bp in length
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* 136766 138277: contig of 1512 bp in length
* 138278 138377: gap of unknown length

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Query Match 5.4%; Score 79.2; DB 2; Length 162797;  
 Best Local Similarity 83.3%; Pred. No. 2e-06;  
 Matches 90; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

QY 682 TGTACTACCTGTTGGAGTCTGCTCAAGTCTTGGCTGGGCTGCGAGGCTACTCTGT 741
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Db 62598 TGTACTACCTGTTGGAGTCTGCTCAAGTCTTGGCTGGGCTGCGAGGCTACTCTGT 62539
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 CTAACCCAGCAGGCTGTTGAGCGGCTCCACCCGTTGTCCTGCTCG 789
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62538 TCTACCCAGCAGGCTGTTGAGCGGCTCCACCCGTTGTCCTGCTCG 62491
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 10  
 AC098981 162797 bp DNA linear HTG 21-DEC-2001  
 LOCUS AC098981  
 DEFINITION Rattus norvegicus clone CH230-112J19, \*\*\* SEQUENCING IN PROGRESS  
 ACCESSION AC098981  
 VERSION AC098981.3 GI:17975740  
 KEYWORDS HTG; HTGS\_PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 162797)  
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

Albrooks,S.L., Amarantune,H.C., Are,J.R., Banks,T., Barbara,J.,  
 Benton,J., Bimarge,K., Blankenburg,K., Bonnin,D., Bouck,J.,  
 Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,  
 Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F.,  
 Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
 Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C.,  
 Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
 Day-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
 Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
 Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,  
 Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,  
 Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,  
 Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,  
 Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,  
 Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,  
 Hollins,B., Homs,F., Howard,S., Huber,J., Huijck,S., Hune,J.,  
 Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,  
 Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryak,J.,  
 Kovar,C., Kratoch,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C.,  
 Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,  
 Louisaged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,  
 Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A.,  
 Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,  
 Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,  
 Morgan,M., Morris,S., Moser,N., Neal,D., Newton,J., Newton,N.,  
 Nguyen,A., Nguyen,S., Nguyen,N., Nickerson,E., Nockenwo,S.,  
 Ogih,M., Okunou,G., Otagunye,N., Oviedo,R., Pace,A., Payton,B.,  
 Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,  
 Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,  
 Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N.,  
 Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,  
 Stone,H., Sutton,A., Swatek,A., Taber,P., Tamerisa,A., Tamerisa,K.,  
 Tang,H., Tansey,J., Taylor,C., Taylor,T., Telitrod,B., Thomas,N.,  
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,  
 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,  
 Wellington,S., Williams,G., Williamson,A., Wlarczyk,R., Woden,S.,  
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
 Weinstein,G. and Gibbs,R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 162797)  
 Morley,K.C.  
 Direct Submission  
 Submitted (08-NOV-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Dec 21, 2001 this sequence version replaced gi:17062421.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GGN2  
 Center clone name: CH230-112J19  
 ----- Summary Statistics  
 Assembly program: Phrap, version 0.990329first call to  
 findphraplist  
 Consensus quality: 12185 bases at least Q40  
 Consensus quality: 132629 bases at least Q30  
 Consensus quality: 141983 bases at least Q20  
 Estimated insert size: 130105; sum-of-coverage estimation  
 Quality coverage: 0x in Q20 bases; agscore-fp estimation  
 Quality coverage: 1.9x in Q20 bases; sum-of-coverage estimation  
 ----- NOTE: Estimated insert size may differ from sequence length  
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 73 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence





JOURNAL  
REFERENCE  
AUTHORSUnpublished  
2 (bases 1 to 70673)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Bana, N., Bastien, V., Boguslavsky, L., Boukingalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P., Deatrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heatford, C., Karats, A., Lacroque, K., Iliev, I., Johnson, R., Jones, C., Karats, A., Lacroque, K., Lamazares, R., Landers, T., Lechoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Petersen, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, D., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Sougne, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (11-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE  
JOURNAL  
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project Information  
Center project name: L13269  
Center clone name: 160\_D1

\* NOTE: This record contains 86 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overall relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 713: contig of 713 bp in length  
\* 714 813: gap of 100 bp  
\* 814 1544: contig of 731 bp in length  
\* 1545 1644: gap of 100 bp  
\* 1645 2364: contig of 720 bp in length  
\* 2365 2464: gap of 100 bp  
\* 2465 3197: contig of 733 bp in length  
\* 3198 3297: gap of 100 bp  
\* 3298 4018: contig of 721 bp in length  
\* 4019 4118: gap of 100 bp  
\* 4119 4821: contig of 703 bp in length  
\* 4822 4921: gap of 100 bp  
\* 4922 5645: contig of 724 bp in length  
\* 5646 5745: gap of 100 bp  
\* 5746 6465: contig of 720 bp in length  
\* 6466 6565: gap of 100 bp  
\* 6566 7300: contig of 735 bp in length  
\* 7301 7400: gap of 100 bp  
\* 7401 8118: contig of 718 bp in length  
\* 8119 8218: gap of 100 bp  
\* 8219 8958: contig of 740 bp in length  
\* 8959 9058: gap of 100 bp  
\* 9059 9738: contig of 680 bp in length  
\* 9739 9838: gap of 100 bp

9839 10506: contig of 668 bp in length  
\* 10507 10606: gap of 100 bp  
\* 10607 11347: contig of 741 bp in length  
\* 11348 11447: gap of 100 bp  
\* 11448 12157: contig of 710 bp in length  
\* 12158 12257: gap of 100 bp  
\* 12258 12953: contig of 696 bp in length  
\* 12954 13053: gap of 100 bp  
\* 13054 13787: contig of 734 bp in length  
\* 13788 13887: gap of 100 bp  
\* 13888 14618: contig of 731 bp in length  
\* 14619 14718: gap of 100 bp  
\* 14719 15463: contig of 745 bp in length  
\* 15464 15563: gap of 100 bp  
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\* 16275 16374: gap of 100 bp  
\* 16375 17086: contig of 712 bp in length  
\* 17087 17186: gap of 100 bp  
\* 17187 17926: contig of 740 bp in length  
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\* 23700 23799: gap of 100 bp  
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\* 25467 26205: contig of 739 bp in length  
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\* 37835 38544: contig of 710 bp in length  
\* 38545 38644: gap of 100 bp  
\* 38645 39357: contig of 713 bp in length  
\* 39358 39457: gap of 100 bp  
\* 39458 40180: contig of 723 bp in length







GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 8, 2002, 07:11:41 : Search time 1612 Seconds

(without alignments)  
12207.344 Million cell updates/sec

Title: US-09-918-359-6

Perfect score: 1458  
Sequence: 1 atgagctcagcctctgtgga.....acctgtgctgtcaggtga 1458

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_lin:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	532.8	36.5	581	9	BE141734 OVO-HT010
C 2	492.6	33.8	499	9	AM177543 RC4-CT015
C 3	415.4	28.5	431	9	AA309878 EST180740
C 4	390	26.7	994	10	BF537032 602048936
C 5	365.2	25.0	410	9	BE168889 QV1-HT051
C 6	358.8	24.6	578	9	AM178598 RC0-HT011
C 7	340	23.3	465	10	BI340329 365560 MA
C 8	329	22.6	1080	10	BG681393 602627753
C 9	309.2	21.2	632	10	BM049977 603624491
C 10	275.8	18.9	350	9	AM814045 RC6-ST019
C 11	270.8	18.6	282	9	AM845954 RC6-ST015
C 12	268.2	18.4	922	10	AM845954 602383354
C 13	267.2	18.3	396	9	AL528343 AL528343
C 14	267.2	17.2	416	9	AV668288 AV668288
C 15	250.4	17.2	489	10	BG385307 306972 MA
C 16	243.2	16.7	1184	10	BI490867 603031843
C 17	241	16.5	894	10	BI456213 603172992

C 18	207.8	14.3	262	9	AM177528 RC4-CT015
C 19	207.6	14.2	673	9	BM216125 BM216125
C 20	178.8	12.3	596	10	BM231050 BM231050
C 21	174	11.9	338	10	BF850563 PM1-EN006
C 22	169.4	11.6	434	9	AM178475 AM178475
C 23	163.6	11.2	852	10	BI107285 BI107285
C 24	151.6	10.4	178	10	BF330244 BF330244
C 25	141.4	9.7	579	9	AM174364 AM174364
C 26	134.6	9.2	691	9	AL632626 AL632626
C 27	101.2	6.9	631	9	AV883460 AV883460
C 28	94.4	6.5	580	9	AL528344 AL528344
C 29	82	5.6	383	10	BF552166 BF552166
C 30	74.8	5.1	507	10	BI855258 BI855258
C 31	68.4	4.7	461	12	AZ854774 AZ854774
C 32	68	4.7	394	10	BI045473 BI045473
C 33	67.2	4.6	341	9	AM322173 AM322173
C 34	63.6	4.4	545	10	BE074505 BE074505
C 35	63.2	4.3	159	9	AM867176 AM867176
C 36	60.8	4.2	833	10	BI160381 BI160381
C 37	59.8	4.1	663	9	AL133778 AL133778
C 38	59.8	4.1	644	10	BG399273 BG399273
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C 40	58.4	4.0	643	9	BB613655 BB613655
C 41	57.8	4.0	579	10	BI682620 BI682620
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C 44	55.6	3.8	619	12	FR0006820 FR0006820
C 45	55.4	3.8	354	12	FR0013559 FR0013559

## ALIGNMENTS

RESULT 1  
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LOCUS OVO-HT0101-061099-032-h12 HT0101 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BE141734  
ACCESSION BE141734  
VERSION BE141734.1 GI:8604455  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 581)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W., Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-QVO-HT0101-061099-032-h12&t3=1999-10-06&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 26  
High quality sequence stop: 580.  
Location/Qualifiers  
1..581  
/organism="Homo sapiens"

FEATURES  
source



LOCUS	AA309878	431 bp	mRNA	linear	EST 19-APR-1997			
DEFINITION	E8180740 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.							
ACCESSION	AA309878							
VERSION	AA309878.1	gi:1962217						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
AUTHORS	1 (bases 1 to 431) Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,V.L., Geoghegan,N.S., Glodde,A., Guelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Macmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Wiley,R., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.							
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence							
JOURNAL	Nature 377 (5547 Suppl), 3-174 (1995)							
MEDLINE	96026280							
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/tdb/hgi.html">http://www.tigr.org/tdb/hgi.html</a> ) Seq primer: M13 Reverse.							
FEATURES	Location/Qualifiers 1..431 /organism="Homo sapiens" /db_xref="ATCC (lnhost):1.155970" /db_xref="taxon:9606" /clone_lib="Jurkat T-cells V" /cell_type="T-lymphocyte" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"							
BASE COUNT	77 a	115 c	120 g	115 t	4 others			
ORIGIN								
Query Match	28.5%; Score 415.4; DB 9; Length 431;							
Best Local Similarity	98.8%; Pred. No. 4.1e-81;							
Matches 416;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
QY	966	CTACTAGCTATTGGCATCATTTGGGATCAACTGTTTGAAGAGCGTCATTTGGCTCTTC	1025					
Db	1	CTACTAGCTATTGGCATCATTTGGGATCAACTGTTTGAAGAGCGTCATTTAGGCTCTTC	60					
QY	1026	TGGAAGACGACGCGCGCCCGCCGCAATGGCTGGCGCGCCCTGGGAGCTCGACGACT	1085					
Db	61	TGGAAGACGACGCGCGCCCGCCGCAATGGCTGGCGCGCCCTGGGAGCTCGACGACT	120					
QY	1086	GGAGTACTGGGCCAACCACTTGATGATTTGGCGGCTGCCCTGGTCACTGTGTGAACCT	1145					
Db	121	GGAGTACTGGGCCAACCACTTGATGATTTTCGGCTGCCCTGGTCACTGTGTGAACCT	180					
QY	1146	GATGTGTGTGAACAACATGGCAGGTGTTTGTGATGATATCGCGGCTACTGAGCCCGTG	1205					

Dp	181	GATGGGCGGAACAACACTGCAGGTGTTTGATGATGATATTCGCGCTACTCAGGCCGCG	240		
Qy	1206	GTCCAAAGATCTATTGTTTGTATTGTGTGGGTGGTGTGTGTGTATCTATCTATGAGTAACCTGTT	1265		
Dd	241				
		GTTCACAGATCACTATTGTTATTTGTGTGGGTGGTGTGTGTGTATCTATCTATGAGTAACCTGTT	300		
Qy	1266	TCTGGCCCTGATTTCTGAGAACCTTCCCTTCACAAAGTGGGACCCCCGACGACCTCTAGCC	1325		
Dd	301				
		TCTGGCCCTGATTTCTGAGAACCTTCCCTTCACAAAGTGGGACCCCCGACGACCTCTAGCC	360		
Qy	1326	CCTTGTGGGACCCAGAGGCCACTTACCAGATGACTGTGAGCTCTGTTCAGGATAT	1385		
Dd	361				
		CCTTGTGGGACCCAGAGGCCACTTACCAGATGACTGTGAGCTCTGTTCAGGATAT	420		
Qy	1386	T	1386		
Dd	421	T	421		
RESULT 4	Bf537032	994 bp	mRNA linear EST 11-DEC-2000		
LOCUS	602048936P1	NCI_CGAP_Sg2	Mus musculus cDNA clone IMAGE:4188321 5'		
DEFINITION	mRNA sequence.				
ACCESSION	Bf537032				
VERSION	Bf537032.1	GI:11624400			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: http://Image.lnl.gov Plate: LHM9512 row: g column: 10 High quality sequence stop: 728. Location/Qualifiers 1. .994 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4188321" /clone_id="NCI_CGAP_Sg2" /lab_host="DH10B (TI phage-resistant)" /note="Organ: salivary gland; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."				
FEATURES	source				
BASE COUNT	247 a	242 c	284 g 221 t		
ORIGIN					
Query Match	26.7%	Score 390:	Dh 10: Length 994;		
Best Local Similarity	76.5%;	Pred. No. 2.2e-75;			
Matches 523;	Conservative 0;	Mismatches 145;	Indels 16; Gaps 3;		
Qy	775	CCGTTGTCCTCTGAGAGCCGAGATGGTGGCCCTGTGTCGTGTGGAGATGACCCGC	834		
Dd	8				
		CCGAGCTCAGATGAGAAGCCAGACGATGATGGCCCACTGTGCTGTGGCATATACACGA	67		
Qy	835	ATGCTGAACATGCTATCCTGCTCCGCTTCTCGGTATCATCCCACATGAAGCCGATG	894		
Dd	68				
		CTGATGAACACACATGATGTGTGTTCCCTTCCCTGGCATCATCCCAACATAAAGCCAATG	127		





Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC0&t2=RC0-HF0112-080999-001-A07&t3=1999-09-08&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 8  
High quality sequence stop: 494.

Db 358 CGGGGGCCTCTCTCAGATGACGGTGGAGCTCTTTTCAGAGGATGTCCTGGAGAGGCCA 417

QY 1400 GGGAGGATGAGCTCACAGAGAGGCTGAGCCACGACCCGCACTGTGGC 1447

Db 418 CGGAGGAGGACCTGATGGAGAAAGCTGAGACCAACCCGACACCTGCACG 465

RESULT	8
BG681393	
LOCUS	1080 bp mRNA linear EST_01-MAY-2001
DEFINITION	602627753n1 NCI-CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752492 5' '
ACCESSION	BG681393
VERSION	BG681393.1 GI:13912790
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sap lens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1080)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: [CGAPs-remail.llnl.gov](mailto:CGAPs-remail.llnl.gov)  
 Tissue Procurement: James Cleaver, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>  
 Plate: LRAM10610 row: j column: 13  
 High quality sequence spot: 829.

FEATURES	Location/Qualifiers
source	1. .1080

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4752492"
/clone_id="NCL_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (p1 phage-resistant)"
/note="Organ: skin; Vector: pCMW-SPOK6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCL_CGAP Library."
BASE COUNT      218 a      295 c      318 g      249 t
ORIGIN

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Query Match	22.6%	Score 329;	DB 10;	Length 1080;
Best Local Similarity	92.0%	Pred. No. 5.8e-62;		
Matches 369; Conservative	0;	Mismatches 30;	Indels 2;	Gaps 2

QY	143	158	203
ACACAGATATGTTGGCAGGACAGGAGAGGCTACCTACTCCAGAACTGGCTTAGTGTTC	ACACAGATATGTTGGCAGGACAGGAGAGGCTACCTACTCCAGAACTGGCTTAGTGTTC	ACACAGATATGTTGGCAGGACAGGAGAGGCTACCTACTCCAGAACTGGCTTAGTGTTC	ACACAGATATGTTGGCAGGACAGGAGAGGCTACCTACTCCAGAACTGGCTTAGTGTTC
143	158	203	266

Db 218 TGACTTCCTCCTGTGCTGCTGACACAGG-CACACACCCGATGTGATGATTCCTCGT 2/

QY 263 ATTCCAAGAACCGGCTATGCCATCTTCTTATAGTCTTCACTGTGATAGGAGACCGT 32

Db 277 ATTCAGAACCGGGCCATGCGATCTTCTCATAGTCTTCACGTGATAGGAACCTGT 33

323 TTCTGATGAACCTGCTGACAGCCATCATCTACAGTCAGTTCGGGGGCTACCTGATGAAAT 38

Db 337 TTCTGATGAACCTGCTGACAGCATCATCTACAGTCAGTTCCGGGGCTACCTGATGAAT 39

383 CTCTCCAGACCTCGCTGTTTCGAGGCGGCTGGGAACCGGGCTGCTTTGAAGTCTAT 44

397, CTCTCCAGACCTCGCTGTTTCGGAGCGGCTGGGAACCCGGCTGCCTTGAAGTCTAT 45

Qy	443	457	Qy	502	Db	517
	CCTCATGTTGGGGAGGAGACCTTTCCTCAGAGC - CACCGCCGACGAGCCGAGATACC	CCTCATGTTGGGGAGGAGAGCCTTTCCTCAGAGCCTTCCTCAGGACATTTGGGGGTGAACCCCAACT		AGCTCTCGTTTCGACAGCGCCGACGATTTCTTTCGGGCAAC		TGCTCTCAGGTCTTCACAGAGTCCACAGTGGACACACTCCCAAC
	501	516	542	557		

RESULT 9	632 bp	mRNA	linear	EST 07-NOV-2001
BM049977				
LOCUS	60362449.1F1	NIH_MGC_40	Homo sapiens	CDNA clone IMAGE:5450134 5',
DEFINITION	mRNA sequence.			
ACCESSION	BM049977			
VERSION	BM049977.1	GI:16779244		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE	1 (bases 1 to 632)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. <a href="mailto:strausberg@mail.nih.gov">strausberg@mail.nih.gov</a>

Email: Cgagap@remail.ru.nl; phone  
funding source: DCM/DG  
CDNA library Preparation: Yang Hong/Rubin Laboratory  
CDNA Library Aried by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Ince genome clones, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
row: 23  
Plate: LNCM938  
High quality sequence step: 627.

FEATURES	Location/Qualifiers
source	1. .632

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5450134"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life
technologies).
Note: this is a NIH_MGC Library."

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Query Match	21.2%	Score 309.2	DB 10	Length 632
Best Local Similarity	99.0%	Pred. No. 1e-57		
Matches 311; Conservative	0	Mismatches 3	Indels 0	Gaps 0

476 AGGCGACCGCGAGGCGCGAGTACCACTCCGTTCTGACAGCGGCCAATCCCTT 53

Db 83 AGAGCACCGCCGAGGCCGAGTCTTCGTTCTGCAGAGCGCCAGTTCCTT 14

QY 536 CGGCACACTACTACTTTGACTACTGGGGAACCTCATGCCCTGGCAAACTGGTGTCCAT 59

Db 143 CGGCACTACTACTTTGACTACTCGGGGAACCTCATCGCCCTGGCAAACTGCTGCAT 20

596 TTGGCTGTTCCTGGTGGTGGATGCGATGTGCTGCTGAGCGTGATGACCTTCATCCT 65

Db  
203 TTGCGTGTCTCTGGATGCAGATGTCTGCTCCCTGCAGCGTGATGACTTCATCTT 26

556 GGGATTCTCAACTGCGTCTTCATTGTGTACTACCTGTTGACGTTGCTGCTCAAGGTCCT 711

Db 263 GGGGATTTCTCAACTGCGCTTCATGTTGACTGTTGAGATGCTGCTCAAGTCTT 322  
 QY 716 TGCCCTGGGCGCTGGAGGGTACCTGCTACCCAGCAACGTTTGAGGGCTCTTAC 775  
 Db 323 TGCCCTGGGCGCTGGAGGGTACCTGCTACCCAGCAACGTTTGAGGGCTCTTAC 382  
 QY 776 CGTTGCTCTGCTGG 789  
 Db 383 CGTTGCTCTGCTGG 396

RESULT 10  
 AM814045 350 bp mRNA linear EST 17-MAY-2000  
 LOCUS  
 DEFINITION RC6-ST0198-081199-021-A12 ST0198 Homo sapiens cDNA, mRNA sequence.  
 AM814045  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 350)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE  
 JOURNAL  
 MEDLINE  
 COMMENT  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=RC6-ST0198-081>)  
 199-021-A12ct3-1999-11-08&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 11  
 High quality sequence stop: 349.  
 Location/Qualifiers

FEATURES  
 source  
 1..350  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="ST0198"  
 /dev\_stage="Adult"  
 /note="Organ: stomach; Vector: puc18; Site:1: SmaI;  
 Site:2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT  
 ORIGIN  
 62 a 102 c 92 g 94 t

Query Match 18.9%; Score 275.8; DB 9; Length 350;  
 Best Local Similarity 99.3%; Pred. No. 1.8e-50;  
 Matches 277; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 476 AGGCGACCGCGAGGCGGAGGACGACGTCGTTTCGACAGGCGCCAGTCTCTT 535  
 11  
 Db 72 AGAGCACCGCGAGGCGGAGGACGACGTCGTTTCGACAGGCGCCAGTCTCTT 131

OY 536 CGGCGACCTACTACTTTGACTTACCTGGGGAACCTATCGCCCTGGCAAACTGGTGCAT 595  
 Db 132 CGGCGACCTACTACTTTGACTTACCTGGGGAACCTATCGCCCTGGCAAACTGGTGCAT 191  
 OY 596 TTGCGTGTTCCTGGTGCATGATGATGTGGCTGTGAGCGGATGATCTTACTCT 655  
 Db 192 TTGCGTGTTCCTGGTGCATGATGATGTGGCTGTGAGCGGATGATCTTACTCT 251  
 OY 656 GGGGATTTCTCAACTGCGCTTCATTTGTTGACTTACCTGTTGAGTTGCTGCTCAAGTCTT 715  
 Db 252 GGGGATTTCTCAACTGCGCTTCATTTGTTGACTTACCTGTTGAGTTGCTGCTCAAGTCTT 311  
 OY 716 TGCCCTGGGCGCTGGAGGGTACCTGCTACCCAGCAA 754  
 Db 312 TGCCCTGGGCGCTGGAGGGTACCTGCTACCCAGCAA 350

RESULT 11  
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 LOCUS  
 DEFINITION RC4-CT0159-130999-001-F01 CT0159 Homo sapiens cDNA, mRNA sequence.  
 AM845954  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 282)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE  
 JOURNAL  
 MEDLINE  
 COMMENT  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=RC4-CT0159-130>)  
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 Seq primer: puc 18 forward  
 High quality sequence stop: 247.  
 Location/Qualifiers

FEATURES  
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 1..282  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="CT0159"  
 /dev\_stage="Adult"  
 /note="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No. 196  
 716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
 BASE COUNT  
 ORIGIN  
 72 a 85 c 75 g 50 t

Query Match 18.6%; Score 270.8; DB 9; Length 282;  
 Best Local Similarity 99.3%; Pred. No. 2e-49;  
 Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1140	GAATTGATGGTGTGTAACAACTGGAGAGGTTTTCGATATGCAATATGAGCGCTACTACAG	1199
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QY	1200	CCCGTGGTCCAAAGATCTATTTTGTATTTGTGTGGCGCTGTCTCTCTCATCTGGGTCAA	1259
Db	214	CCCTGGTCCAAAGATCTATTTATTTATTTGTGTGGCGCTGTCTCTCATCTGGGTCAA	155
QY	1260	CCGTCTTCTGGCCCTGATTTCTGTGGAGAACTCCCTTCAAGTGGAGCCCGGACGACACT	1319
Db	154	CTGTGTTCTGGCCCTGATTTCTGTGGAGAACTTCTTCAAGTGGAGCCCGGACGACACT	95
QY	1320	GCAGCCCCCTTGTGGAGCCCCAGAGGCCACTACAGATGACTGTGTGAGCTCTCTTTAG	1379
Db	94	GCAGCCCCCTTGTGGAGCCCCAGAGGCCACTACAGATGACTGTGTGAGCTCTCTTTAG	35
QY	1380	GGATATTCTGGAGGAGCCCGGGGAGATGAGCTC	1413
Db	34	GGATATTCTGGAGGAGCCCGGGGAGATGAGCTC 1	

RESULT 12			
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LOCUS	RG286144	922 bp	RNA
DEFINITION	60238354P1 NIH_MGC_94	Mus musculus	CDNA clone IMAGE:450097 5',
DESCRIPTION	mRNA sequence.		

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	GI:13038768
BG286144	
BG286144.1	
EST.	
house mouse.	
Mus musculus	

REFERENCE  
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus:  
1 (bases 1 to 922)  
NIH-MGC <http://mgc.ncl.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

CDNA library Preparation: Life Technologies, Inc.  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10367 row: k column: 14  
High quality sequence stop: 694.

**FEATURES**  
**SOURCE**

1. .922

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/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone="IMAGE:4500997"
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/lab.host="DH10B (phage-resistant)"
/notes="Orgn: eye: Vector: pcwv-SpOrt6; site.1: NotI;
site.2: SalI; Cloned unidirectionally; oligo-ctf primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH-MGC library."

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BASE COUNT  
ORIGIN

178 a 231 c 270 g 243 e

Query Match	18.4%	Score 268.2	DB 10	Length 922
Best Local Similarity	71.0%	Pred. No. 1.2e+48		
Matches 384: Conservative	0	Mismatches 153	Indels 4	Gaps 2

**OY** 788 GGAAGCGGAGATGGTGGCCCTCCTGTGTGGCATATACCCGCATGTGAACAATGC 847  
||||| |||| | |||| | |||| | |||| | |||| |  
**Dd** 244 GGAAGCAGACAGCAAGTAGTGCCACCACGTGGCTGTGGACATGACACGACTGTATGAACAC 3033  
||||| |||| | |||| | |||| | |||| | |||| |  
**PY** 849 TCATCGTTCCGCTTCCTGCGTATCATCCCCAGCATGAAGCCGATGGCGTGGTGCCA 907

Db	304	TGATTGTTTCCTCCTCGGCATCATCCCAACATAAAGCCAAATGGCTGAGGTAGCA	363
Qy	908	GTACCGTCCTGGCCCTGGTGAGAACATGCGTGGCTTGGCGGATCCTGCTGGTCT	967
Db	364	ACACCATCTCGGCGCTAATCCCTAACTGAGGGCATTTGGGAGATCCTGGTGGCAT	423
Qy	968	ACTAGCTATTTGGCCATCATTTGGATGCAACTGTTTAGAGGCTCATTTGGCTTTCCTG	1027
Db	424	ACTATGTTTGTGGCCATGATCGGATCAACCTGTTCCAGAGTGATATGCTG---CCTCTG	480
Qy	1028	GAACAGCAGCGCTGGCCCTCGCCATGAGCTCGGCGCCCTGTGGAGCTTTCGACAGCTGG	1087
Db	481	GAACAGCAGCGCTGGTTTCCCGACAAACATCAAGCTGATGTGGAAGCTTTGACGAGCTAG	540
Qy	1088	AGTACTGGCCCAACACTTCGATGACTTTGGCGCTGGCCCTGCTACCTCTGTGGAACTTGA	1147
Db	541	GTTACTGGCGCCCAACACTTTGACGACTTTGGCTGGCTTTATCACTGTGGAACTGGA	600
Qy	1148	TGGTGTTGAACACAGCGAGGTGTTTGGAATGATATCGGCGCTACTACGAGCCGCTGGT	1207
Db	601	TGGTGTTGAACATTTGGCAGGTGATCTCGGAAGCTATAAGGCGTAGCAGAGCGCGTGGT	660
Qy	1208	CCAAATCATTTTGTATTTGTGGTGGCTGGTGTCTGTGCATCTGGGTCAACCTGTTTC	1267
Db	661	CATAGGTGTA-TTTGTGCTATGCTGGTGGTGTCTCTGTATCTGGAATCCACGCTGTTT	719
Qy	1268	TGGCCCTGATTTTGGAGAACTTCTTACAAAGTGGAGACCCCGCAGCCACCTGCGAGGCC	1327
Db	720	CTGGGTTCTCTTTCGAGAACCTTTTCCACGAATGGAGCCCTCAAGGTCTAAGAGCTTC	779
Qy	1328	T 1328	
Db	780	T 780	

RESULT 13	AL528343	396 bp	mRNA	linear	EST 13-FEB-2001
LOCUS	AL528343	LTI_NFL003_NBC3	Homo sapiens	cDNA clone CS00C023yP19.3	
DEFINITION	pr1me, mRNA sequence.				
ACCESSION	AL528343				
VERSION	AL528343.1	GI:12791836			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1. (bases 1 to 396)				
AUTHORS	Li, W.-B., Gruber, C., Jesssee, J. and Polayars, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				

FEATURES  
source

1. .396

3

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/organism="Homo sapiens"  
/db_xref="taxon:9606"
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/clone="CS0DC023YP19"  
/clone_11b="LTI_NFL003_NBC3"
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/crone_lib= E11_NE0003_NBC3
/sex="male"
/tissue type="neuroblastoma cells"

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/tissue_type="neuroblastoma cells"
/lab_host="DH10B"

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and Eco RV sites of the pcMVSPORT 6 cloned into the Not I and Eco RV sites of the pcMVSPORT 6

Library was constructed by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center  
by Life Technologies. Contact : Feng Liang Lile  
Building 20850, Marland USA Fax : (1) 301 610  
Daring Rockville

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610













QY 960 ----- 959  
Db 1847 CTGGGCTGACCCAGCTGTGCTCGCGCTGTGAAATAGAGCTGGAGAGATCTT 1906  
QY 960 ----- 959  
Db 1907 GCCTCAGTGTCTGTCCCGCCCTTAATTGCACAGCAGAGAACTGAGGCCAGA 1966  
QY 960 ----- 959  
Db 1967 AAGGGAGCAGGTGTCTACTACTGATTTGGCATCATTTGGGATCACTGTTTAGAGGCG 2026  
QY 1010 TCATTTGGCTCTCTCTCGAAGACAGAGCTGGCCCTTCCCAATGGCTGGGCGCTGTG 1069  
Db 2027 TCATTTGGCTCTCTCTCGAAGACAGAGCTGGCCCTTCCCAATGGCTGGGCGCTGTG 2086  
QY 1070 GGAGCTTCAGACAGCTGAGTACTGGGCGCAACAATTGATGCTGGGCTGGCCCTGG 1129  
Db 2087 GGAGCTTCAGACAGCTGAGTACTGGGCGCAACAATTGATGCTGGGCTGGCCCTGG 2146  
QY 1130 TCATCTGTGGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1189  
Db 2147 TCATCTGTGGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2206  
QY 1190 GCTACTAGGCGCGTGTGTCACAGATCTATTTGATGATGATGATGATGATGATGATG 1249  
Db 2207 GCTACTAGGCGCGTGTGTCACAGATCTATTTGATGATGATGATGATGATGATGATG 2266  
QY 1250 TCTGGTTCACACCTGTTTCTGGCCCTGATCTGAGAACCTCTCTCAACAGTGGAGCCCG 1309  
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Db 2327 GCAGCCACCTGACAGCCCTTCTGAGAGACCCCAAGAGCCAGTCCAGATGATGATGAG 2386  
QY 1370 TCCGTTTCAGAGGATATCTGAGAGAGCCCGGAGATGATGATGATGATGATGATGATG 1429  
Db 2387 TCCGTTTCAGAGGATATCTGAGAGAGCCCGGAGATGATGATGATGATGATGATGATG 2446  
QY 1430 AGCACCAGCAGCTGTGCTGTGAGGTGA 1458  
Db 2447 AGCACCAGCAGCTGTGCTGTGAGGTGA 2475

RESULT 3  
ID AAV59758 standard; DNA: 2377 BP.  
XX AAV59758;  
AC AAV59758;  
XX AAV59758;  
DT 19-JAN-1999 (first entry)  
XX Human secreted protein gene 100 clone HEONN58.  
DE Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW Immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW Inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO9839448-A2.  
XX 11-SEP-1998.  
XX 06-MAR-1998; 98WO-US04493.  
XX

PR 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043314.  
PR 11-APR-1997; 97US-0043568.  
PR 11-APR-1997; 97US-0043569.  
PR 11-APR-1997; 97US-0043576.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043669.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0047492.  
PR 23-MAY-1997; 97US-0047500.  
PR 23-MAY-1997; 97US-0047501.  
PR 23-MAY-1997; 97US-0047502.  
PR 23-MAY-1997; 97US-0047503.  
PR 23-MAY-1997; 97US-0047581.  
PR 23-MAY-1997; 97US-0047582.  
PR 23-MAY-1997; 97US-0047583.  
PR 23-MAY-1997; 97US-0047584.  
PR 23-MAY-1997; 97US-0047585.  
PR 23-MAY-1997; 97US-0047586.  
PR 23-MAY-1997; 97US-0047587.  
PR 23-MAY-1997; 97US-0047588.  
PR 23-MAY-1997; 97US-0047590.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047593.  
PR 23-MAY-1997; 97US-0047594.  
PR 23-MAY-1997; 97US-0047595.  
PR 23-MAY-1997; 97US-0047596.  
PR 23-MAY-1997; 97US-0047597.  
PR 23-MAY-1997; 97US-0047598.  
PR 23-MAY-1997; 97US-0047599.  
PR 23-MAY-1997; 97US-0047600.  
PR 23-MAY-1997; 97US-0047601.  
PR 23-MAY-1997; 97US-0047612.  
PR 23-MAY-1997; 97US-0047613.  
PR 23-MAY-1997; 97US-0047614.  
PR 23-MAY-1997; 97US-0047615.  
PR 23-MAY-1997; 97US-0047617.  
PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
PR 23-MAY-1997; 97US-0047633.  
PR 06-JUN-1997; 97US-0048964.  
PR 06-JUN-1997; 97US-0048974.  
PR 13-JUN-1997; 97US-0049610.  
PR 08-JUL-1997; 97US-0051926.  
PR 16-JUL-1997; 97US-0052874.  
PR 18-AUG-1997; 97US-0055724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056862.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.

IID	AAH9106 standard; CDNA; 1734 BP.
XX	
XX	
AC	AAH9106;
XX	
XX	
DT	12-OCT-2001 (first entry)
XX	

DE Human EST-derived coding sequence SEQ ID NO: 963.  
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.  
 OS Homo sapiens.  
 XX WO200154477-A2.  
 XX 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02687.  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 PI WPI: 2001-476164/51.  
 DR P-PSDB; AAM24447.  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 PS Claim 1: Page 756-757; 1275pp; English.  
 XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 XX Sequence 1734 BP; 315 A; 451 C; 531 G; 436 T; 1 other;  
 SO  
 Query Match 51.6%; Score 752.4; DB 22; Length 1734;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-176;  
 Matches 753; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 368 CCTGTGGAGCTTCGACACACTGGAGTACGCGCAACAACCTTCGACTTTCGCGTG 427  
 QY 1124 CCTGTGCTACTCTGTGGAACCTTGTATGTTGTAACAACCTGGAGGTTTGTGATGCAT 1183  
 DB 428 CCCGGGCTACTCTGTGGAACCTTGTATGTTGTAACAACCTGGAGGTTTGTGATGCAT 487  
 QY 1184 ATGGGCTACTCTGAGCGCCGTGGTCCAAAGATCTATTTGTATGTTGTTGCTGCTGCT 1243  
 DB 488 ATGGGCTACTCTGAGCGCCGTGGTCCAAAGATCTATTTGTATGTTGTTGCTGCTGCT 547  
 QY 1244 CTGTCACTGTGGTCAACCTGTTTGTGCTGATTTCTGGAACCTTCTTCAAACTGGG 1303  
 DB 548 CTGTCACTGTGGTCAACCTGTTTGTGCTGATTTCTGGAACCTTCTTCAAACTGGG 607  
 QY 1304 ACCCGCGAGCCACTGAGCCCTTCTGAGAGCCCGAGAGCCACTTACAGATGACTG 1363  
 DB 608 ACCCGCGAGCCACTGAGCCCTTCTGAGAGCCCGAGAGCCACTTACAGATGACTG 667  
 QY 1364 TGAGCTCTCTGTCAGGATATTTCTGAGAGAGCCCGGAGGATGAGCTTCAGAGAGCC 1423  
 DB 668 TGAGCTCTCTGTCAGGATATTTCTGAGAGAGCCCGGAGGATGAGCTTCAGAGAGCC 727  
 QY 1424 TGAGCCAGCACCCTGAGCTGTGCTGTGCAAGTGA 1458  
 DB 728 TGAGCCAGCACCCTGAGCTGTGCTGTGCAAGTGA 762  
 RESULT 5  
 ID AAV59610 standard; DNA; 1751 BP.  
 AC AAV59610;  
 AC AAV59610;  
 DE 06-JAN-1999 (first entry)  
 XX Human secreted protein gene 100 clone HLGAB52.  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 OS Homo sapiens.  
 XX WO9839448-A2.  
 XX 11-SEP-1998.  
 PD 06-MAR-1998; 98WO-US04493.  
 XX 02-OCT-1997; 97US-0061060.  
 PR 07-MAR-1997; 97US-0038621.  
 PR 07-MAR-1997; 97US-0040161.  
 PR 07-MAR-1997; 97US-0040162.  
 PR 07-MAR-1997; 97US-0040163.  
 PR 07-MAR-1997; 97US-0040333.  
 PR 07-MAR-1997; 97US-0040334.  
 PR 07-MAR-1997; 97US-0040336.  
 PR 07-MAR-1997; 97US-0040626.  
 PR 11-APR-1997; 97US-0043311.  
 PR 11-APR-1997; 97US-0043312.  
 PR 11-APR-1997; 97US-0043313.  
 PR 11-APR-1997; 97US-0043314.  
 PR 11-APR-1997; 97US-0043568.  
 PR 11-APR-1997; 97US-0043569.  
 PR 11-APR-1997; 97US-0043576.  
 PR 11-APR-1997; 97US-0043578.  
 PR 11-APR-1997; 97US-0043580.













CC calcium channel alpha-1 subunit operably linked to control sequences  
 CC to effect its expression. The novel calcium channel nucleic acids and  
 CC proteins are useful for treating conditions characterised by  
 CC undesirable levels of T-type calcium channel activity such as cardiac  
 CC hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
 CC epilepsy.

SO Sequence 1608 BP; 261 A; 528 C; 522 G; 297 T; 0 other;

Query Match 4.1%; Score 60; DB 22; Length 1608;  
 Best Local Similarity 47.6%; Pred. No. 5.2e-05;  
 Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

```

OY 531 CTCTTGGGCGGCTACTACTTGTGACCTGGGGAACCTCATCGCCCTGGCAACCTGGTG 590
    || || || || || || || || || || || || || || || || || || || || || ||
DB 339 CTGCTGTGCAACCCATGCTGTTGAGACAGCTGACATGCTGTATCATGCTCAACGCGTG 398
OY 591 TCCATTGGCTGTCTCTGCTGTGATGACAGATGCTGCTGCTGAGCGCTGATGACTTC 650
    || || || || || || || || || || || || || || || || || || || || || ||
DB 399 ACCCTGGGATGTTCCGGCCCTGTGAGACGTTGAGTGGCGCTCCGAGCG--CTGCAC 455
OY 651 ATCCCTGGGATGCTCAACGCGCTTCATGTTGTAATCACTACCTTTGGAGTGTGCTGCAAG 710
    || || || || || || || || || || || || || || || || || || || || || ||
DB 456 ATCTGGAGGCTTTGACGCTTCATTTTCGCTTTTTCGCTGAGAGATGCTCAATCAG 515
OY 711 GTCTTGGCCCTGGGCTGGAGAGGTACTGCTTACCCAGACAGCTGTTTGGAGGCTC 770
    || || || || || || || || || || || || || || || || || || || || || ||
DB 516 ATGTGCGCTTGGGCTGTGTCGGGAGAGTGTACCTGGGAGACAGTGGAAACAGCGTG 575
OY 771 CTCACCGTGTCTGCTGAGAGCGGAGATGCTGCTGCTGCTGCTGCTGAGACATGAC 830
    || || || || || || || || || || || || || || || || || || || || || ||
DB 576 GATTTCATGCTGCTGAGCGGAGC-ATGATGAGATGACTGTTGAGACGAGACACAGCTGAG 634
OY 831 CCGCATGTGAGACATGCTATGCTGTTCCGCTTCCGCTATCATCATCCAGCATGAGCC 890
    || || || || || || || || || || || || || || || || || || || || || ||
DB 635 CCGCTGGCTATAGACCG-----TGGGGTGTCTGGGCGCCCTCCGCGCATCACCG 688
OY 891 GATGGCGTGTGGGCGGAGTACCTGCTGGGCGTGTGAGCAACATGCTGCTGGCGG 950
    || || || || || || || || || || || || || || || || || || || || || ||
DB 689 CGTGCGTATGAGATCGGATCCTGTGTACCTGCTGCTGAGATGAGTGGCCATGCTGGGAA 748
OY 951 GATCTGCTGTGTGTCTACTACTATTTGCAATGTTGGAGATCACTTTTAAAGGCT 1010
    || || || || || || || || || || || || || || || || || || || || || ||
DB 749 CGTCTCTGTGCTGCTTCTTCTCTTCTTCAATTTTGGGATGTTGGGCTCAAGCTTG 808
OY 1011 CATTTGGGCTCTCTCTGAAACAGACAGCTGGGCGCTGCAATGCTGGCGCCCTGTGG 1070
    || || || || || || || || || || || || || || || || || || || || || ||
DB 809 GGGTGGCTCTCTGGAACCGCTGCTCTGAGACAGTGGCTTTGTGAGAACACACACT 868
OY 1071 GAGCTTCGAGCAGCTGAGTACTGGGCCAACAACTTCGATGA 1112
    || || || || || || || || || || || || || || || || || || || || || ||
DB 869 GACCTTCCTGCGGCGCTACTACCAAGAGAGAGGCGGAGGA 910

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## RESULT 12

AAK83490  
 ID AAK83490 standard; cDNA; 6114 BP.

XX AAK83490;

DT 07-DEC-1999 (first entry)

XX Human T-type voltage-gated Ca channel alpha-1-H (hcaV12b) cDNA.

XX Human: T-type voltage-gated calcium channel; membrane; pore; ion;

KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

OS Homo sapiens.

XX WO929847-A1.

XX 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US23161.  
 PR 05-DEC-1997; 97US-0985809.  
 XX (JOYO) UNIV LOYOLA CHICAGO.  
 FA  
 XX Perez-Reyes E, Cribbs LL;  
 PI  
 XX WPI: 1999-394972/33.  
 DR P-PSDB: AA14595.  
 XX  
 PT New T-type voltage-gated calcium channels -  
 PS Disclosure; Page 111-119; 138pp; English.

CC This sequence represents the coding region for a human T-type  
 CC voltage-gated calcium (Ca) channel alpha-1-H designated hcaV12b.  
 CC Voltage-gated channels are membrane bound glycosylated proteins formed of  
 CC several subunits. The large alpha subunits form a pore in the membrane  
 CC that is selective for a given ionic species. Each alpha subunit contains  
 CC 4 domains (I, II, III and IV) and each domain contains 6 putative  
 CC transmembrane helical segments (S1-S6). T-type Ca channels are  
 CC activated at a lower voltage than L- or N-type channels. Characteristics  
 CC of T-type channels include short current time, slow activation kinetics  
 CC near threshold, fast inactivation kinetics and slow tail current. The  
 CC sequences AAK83481-X83492 represent novel T-type voltage-gated Ca  
 CC channel genes from humans and rats. Each of the novel Ca-channels  
 CC contains a putative IVS4 region comprising the amino acid sequence  
 CC AA14598. Cells expressing the T-type voltage-gated calcium channel  
 CC proteins can be used to screen for drugs which affect calcium channels.  
 CC Methods are also disclosed for treating a disease or disorder associated  
 CC with a deficiency in a native T-type calcium channel nucleic acid, e.g.  
 CC to treat cardiomyopathy, epilepsy, etc.

SO Sequence 6114 BP; 1056 A; 2047 C; 1894 G; 1117 T; 0 other;

Query Match 4.1%; Score 60; DB 20; Length 6114;  
 Best Local Similarity 47.6%; Pred. No. 8.4e-05;  
 Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

```

OY 531 CTCTTGGGCGGCTACTACTTGTGACCTGGGGAACCTCATCGCCCTGGCAACCTGGTG 590
    || || || || || || || || || || || || || || || || || || || || || ||
DB 293 CTGCTGTCAACCCATGCTGTTGAGACAGCTGACATGCTGTATCATGCTCAACGCGTG 342
OY 591 TCCATTGGCTGTCTCTGCTGTGATGACAGATGCTGCTGCTGAGCGTATGACTTC 650
    || || || || || || || || || || || || || || || || || || || || || ||
DB 343 ACCCTGGGATGTTCCGGCCCTGTGAGAGCTTGAAGCGGCTCCGAGCG--CTGCAC 399
OY 651 ATCCCTGGGATGCTCAACGCGCTTCATGTTGTAATCACTACCTTTGGAGTGTGCTGCAAG 710
    || || || || || || || || || || || || || || || || || || || || || ||
DB 400 ATCTGGAGGCTTTGACGCTTCATTTTTCGCTTTTTCGCTGAGAGATGCTATCAAG 459
OY 711 GTCTTGGCCCTGGGCTGGAGAGTACTGCTTACCCAGACAGCTGTTTGGAGGCGCTC 770
    || || || || || || || || || || || || || || || || || || || || || ||
DB 460 ATGTGCGCTTGGGCTGTGCGGAGAGATGTTACTGCTGGTGTGACAGTGGAAACAGCGTG 519
OY 771 CTCACCGTGTGTCTGCTGAGAGCGGAGATGCTGCTGCTGCTGCTGCTGAGACATGAC 830
    || || || || || || || || || || || || || || || || || || || || || ||
DB 520 GATTTCATGCTGCTGCTGCGGCGG-ATGATGAGATGCTGCTGAGAGACACAACTGAG 578
OY 831 CCGCATGTGAAACATGCTATGCTGTTCCGCTTCCGCTGATCATATCCCAAGCATGAGCC 890
    || || || || || || || || || || || || || || || || || || || || || ||
DB 579 CCTCTCGGCTATACAGACG-----TGGGGTGTCTGGGCGCCCTCCGCGCATCAACCG 632
OY 891 GATGGCGTGTGGGCGGAGTACCTGCTGGGCGTGTGAGCAACATGCTGCTTGGCGG 950
    || || || || || || || || || || || || || || || || || || || || || ||
DB 633 CGTGCGTATGAGATCGGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
OY 951 GATCTGCTGTGTGTCTACTACTATTTGCAATGTTGGAGATCACTTTTAAAGGCT 1010
    || || || || || || || || || || || || || || || || || || || || || ||
DB 693 CGTCTCTGCTGCTGCTTCTTCTTCTTCAATTTTGGGATGCTGCTGCTGCTGCTGCTG 752
OY 1011 CATTTGGGCTCTCTCTGAAACAGAGCGTGGCGCCCTCCAAATGCTGGCGGCGCTGTGG 1070

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PT Subunits of calcium channels  
 XX Claim 1(c): Page 162-171; 171pp; English.  
 PS This is the nucleotide sequence of cDNA coding for the alpha 1H-2  
 CC subunit (see AAY06300) of a human low-voltage activated calcium  
 CC channel. The cDNA was obtained by PCR amplification from a Tt cell  
 CC cDNA library. The invention provides calcium channel subunits,  
 CC including 2 splice variants of alpha 1H-1 (see AAX59080 and AAX59081),  
 CC and isoform alpha 1H-2. The 1H-2 isoform contains a 957 nucleotide  
 CC deletion relative to alpha 1H-1, resulting in a loss of 319 amino  
 CC acids within the intracellular loop between domains II and III.  
 CC The splice variant deletion was identified by PCR in all cells and  
 CC tissues examined. These included Tt cells, amygdala, caudate  
 CC nucleus, putamen, heart, kidney and liver cells. Cells and vectors  
 CC containing these nucleic acids, and methods for identifying  
 CC compounds that modulate the activity of calcium channels that  
 CC contain these subunits are provided by the invention. Such  
 CC compounds are used to treat calcium channel mediated disorders,  
 CC including neurological, endocrinological, cardiovascular,  
 CC urological, hepatic, respiratory and vascular disorders.  
 XX  
 XX Sequence 6941 BP; 1146 A; 2333 C; 2225 G; 1237 T; 0 other;  
 SQ  
 Query Match 4.1%; Score 60; DB 20; Length 6941;  
 Best Local Similarity 47.6%; Pred. No. 8.8e-05;  
 Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

QY 531 CTCTTGGCCACTACTACTGAGTGGGAACTCAGTCCCTGGCAACCTGGTG 590  
 DB 534 CTGCTCTGCACCCATGCTGAGCAGCATGCTGTAATCATCTCAACCTGCTG 593  
 QY 591 TCCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 650  
 DB 594 ACCCTGGGATGCTGGGCTGTGAGACGTTGAGTGGGCTCCGACG---CTGCAC 650  
 QY 651 ATCTGGGGATTCATCACTGCTCTTCACTTGTACTACTCTGTTGAGAGTGGTCTGCTCAAG 710  
 DB 651 ATCTGGAGAGGCTTGGAGCCCTTCACTTGTGGCTTTTGGGATGATGGTCAAG 710  
 QY 711 GCTTTGGCCCTGGGCTGGAGAGTACCTGCTCTCAACCCAGAACAGTGTAGAGGGCTG 770  
 DB 711 ATGCTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 770  
 QY 771 CTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830  
 DB 771 GATTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829  
 QY 831 CCGCATGCTGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890  
 DB 830 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883  
 QY 891 GATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 950  
 DB 884 CGTCTTACATGCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 943  
 QY 951 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010  
 DB 944 CGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003  
 QY 1011 CATTTGGCTCTTCTGGAACAGACGCTGGCCCTGCGCAATGGCTGGCCCTGTGG 1070  
 DB 1004 GGTCTGCTCTCTGCGGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063  
 QY 1071 GAGCTTGGAGAGCTGAGTACTGGGCGCAACACTTGCATGA 1112  
 DB 1064 GACTTCTGCTGCGGCTGCTACTACAGAGGAGGAGGAGGA 1105

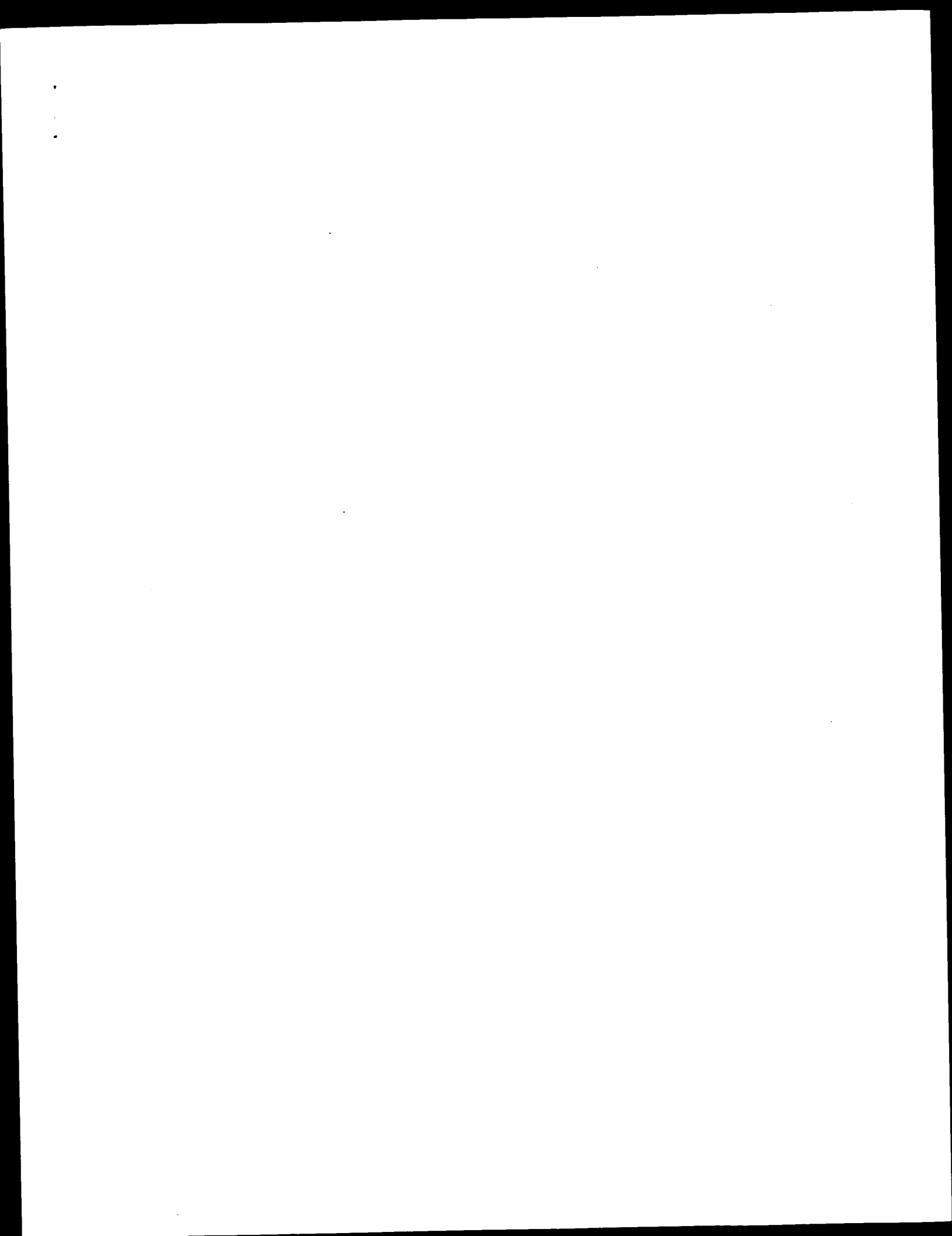
RESULT 15  
 AAX59080  
 ID AAX59080 standard; cDNA; 7898 BP.  
 XX

AC AAX59080;  
 XX  
 DT 23-AUG-1999 (first entry)  
 XX  
 DE Human activated calcium channel alpha 1H-1 subunit cDNA.  
 XX  
 KW Calcium channel subunit 1H-1; human; neurological disorder;  
 KW endocrinological disorder; cardiovascular disorder;  
 KW urological disorder; hepatic disorder; respiratory disorder;  
 KW vascular disorder; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 249..7310  
 FT /tag= a  
 FT  
 XX  
 PN W0928342-A2.  
 XX  
 PD 10-JUN-1999.  
 PD  
 XX  
 PF 03-DEC-1998; 98WO-US25671.  
 XX  
 PR 10-NOV-1998; 98US-018932.  
 PR 03-DEC-1997; 97US-0984709.  
 PR  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Hans M, Harpold M, Stauderman K, Urrutia A, Washburn MS;  
 PI Williams M;  
 XX  
 XX WPI; 1999-371096/31.  
 DR P-PDB; AAY06298.  
 XX  
 PT Subunits of calcium channels  
 XX  
 PS Claim 1(c): Page 138-149; 171pp; English.  
 XX  
 CC This is the nucleotide sequence of cDNA coding for the alpha 1H-1  
 CC subunit (see AAY06298) of a human low-voltage activated calcium  
 CC channel. This full-length cDNA sequence was deduced from  
 CC overlapping partial clones isolated from a Tt cell cDNA library.  
 CC The invention provides calcium channel subunits, including 2 splice  
 CC variants of alpha 1H-1 (see also AAX59081), and isoform alpha 1H-2  
 CC (see AAX59082). The 1H-1 splice variants were detected by RT-PCR  
 CC in multiple tissues. They differ only at codon 2230, being either  
 CC GAC (Asp) or GAA (Glu). 1H-2 has a 957 nucleotide deletion in the  
 CC I-II intracellular loop when compared with 1H-1. Cells and vectors  
 CC containing these nucleic acids, and methods for identifying  
 CC compounds that modulate the activity of calcium channels that  
 CC contain these subunits are provided by the invention. Such  
 CC compounds are used to treat calcium channel mediated disorders,  
 CC including neurological, endocrinological, cardiovascular,  
 CC urological, hepatic, respiratory and vascular disorders.  
 CC  
 XX  
 SQ Sequence 7898 BP; 1319 A; 2694 C; 2538 G; 1347 T; 0 other;  
 Query Match 4.1%; Score 60; DB 20; Length 7898;  
 Best Local Similarity 47.6%; Pred. No. 9.2e-05;  
 Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

QY 531 CTCTTGGCCACTACTACTGAGTGGGAACTCAGTCCCTGGCAACCTGGTG 590  
 DB 534 CTGCTCTGCACCCATGCTGAGCAGCATGCTGTAATCATCTCAACCTGCTG 593  
 QY 591 TCCATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 650  
 DB 594 ACCCTGGGATGCTGGGCTGTGAGACGTTGAGTGGGCTCCGACG---CTGCAC 650  
 QY 651 ATCTGGGGATTCATCACTGCTCTTCACTTGTACTACTCTGTTGAGAGTGGTCTGCTCAAG 710  
 DB 651 ATCTGGAGAGGCTTGGAGCCCTTCACTTGTGGCTTTTGGGATGATGGTCAAG 710

QY 711 GTCCTTGGCCCTGGCCCTGGAGGATACCTGTCCTCCAGCAACGTTGAGGGCTC 770  
Db 711 ATGGTGGCCTTGGGGCTGTTCCGGGCAGAACTGTACCTGGGTGACAGTGGAAACAGGCTG 770  
QY 771 CTCACCGTTTCCTGCTGGAGGCCGGAGATGTGGGCCCTGCTGCTGTGGGACATGAC 830  
Db 771 GATTTCTTCAATCGTGGGGGGC-ATGATGAGTACTGCTTGGAGGACACACACTGAG 829  
QY 831 CCGCATGCTGACATGCTCATGCTGTCGCTTCCTGCGTATGATCCCAAGCATGAGCC 890  
Db 830 CTTCTGGGCTATCAGGACCG-----TGGGGGTGCTGGGGCCCTCCGGCCATCAACCG 883  
QY 891 GATGGCCGTGGTGGCCAGTACCGTCCCTGGGCCCTGGTGCAGAAACATGCGGTTGGGGG 950  
Db 884 CGTCCCTAGCATGCGGATCTGTGCTCACTCGCTGCTGATACGCTGCCATGCTCGGGA 943  
QY 951 GATCCTGTGTGTGCTACTAGTATTTGCCATGATGGATCAACTGTTAGAGGCGT 1010  
Db 944 CGTCCCTGTGTGTGCTTCTTGTCTTCTTCAATTTCCGATGCTGGGCTCAGCTCTG 1003  
QY 1011 CATGTGGCTTCTCTGAAACAGCAGAGCTGGCCCTGGCCATGGCTGGGCCCTGTGG 1070  
Db 1004 GGCTGGCCCTCTGCGAAACCGCTGCTCTCTGACAGTGGCTTTGTAGAGAACACACACT 1063  
QY 1071 GAGCTTCGAGCAGCTGGAGTACTGGGCCACACACTTGCATGA 1112  
Db 1064 GACCTTCCCTGGCGGCTACTACAGACGAGGAGGCGAGGA 1105

Search completed: October 8, 2002, 08:09:01  
Job time : 222 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 08:02:31 : Search time 51 seconds  
(without alignments)  
7022.228 Million cell updates/sec

Title: US-09-918-359-6

Perfect score: 1458

Sequence: 1 atgagctcagcctctgtgga.....acctgtgtgtgtgaggtga 1458

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTCUTS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	4.1	7898	4	US-08-984-709A-49
2	51.4	3.5	1669	4	US-08-984-709A-51
3	50.6	3.5	5975	1	US-08-404-354B-1
4	50.6	3.5	5975	1	US-08-314-083B-1
5	50.6	3.5	5975	1	US-08-435-675B-1
6	50.6	3.5	5975	1	US-08-336-257A-3
7	50.6	3.5	5975	1	US-08-884-599-1
8	49.2	3.4	6816	4	US-09-404-650-1
9	49.2	3.4	6855	4	US-09-404-650-3
10	47.4	3.3	5962	6	5386025-5
11	45.8	3.1	6048	4	US-09-634-920-3
12	45.8	3.1	6503	4	US-09-404-650-12
13	45.6	3.1	7218	1	US-08-232-463-14
14	43.8	3.0	3489	2	US-08-728-323A-1
15	43.8	3.0	6822	4	US-09-426-998-3
16	43.8	3.0	7741	4	US-09-426-998-4
17	43.8	3.0	32207	2	US-08-770-379-20
18	43.8	3.0	32207	4	US-08-757-669A-20
19	43.8	3.0	32207	4	US-09-230-371A-20
20	42.6	2.9	1138	3	US-08-581-146C-3
21	41.2	2.8	2338	2	US-08-455-543A-31
22	41.2	2.8	2338	2	US-08-223-305C-31
23	41.2	2.8	5904	1	US-07-745-206A-6
24	41.2	2.8	5904	1	US-08-455-543A-3
25	41.2	2.8	5904	2	US-08-193-076B-3
26	41.2	2.8	5904	2	US-08-223-305C-3
27	41.2	2.8	5904	2	US-08-149-097D-3

28	41.2	2.8	5904	2	US-08-311-363-6	Sequence 6, Appl
29	41.2	2.8	6575	3	US-08-949-386-3	Sequence 3, Appl
30	41.2	2.8	6575	3	US-08-450-562-3	Sequence 3, Appl
31	41.2	2.8	6575	4	US-08-984-709A-3	Sequence 3, Appl
32	40.2	2.8	1901	1	US-08-153-848-43	Sequence 43, Appl
33	40.2	2.8	1901	1	US-09-299-845A-43	Sequence 43, Appl
34	40.2	2.8	1901	4	US-09-088-337B-43	Sequence 43, Appl
35	40.2	2.8	1901	5	PCR-US93-1153-43	Sequence 43, Appl
36	40.2	2.8	2453	5	PCR-US95-07180-1	Sequence 1, Appl
37	40.2	2.8	2742	4	US-09-232-468A-1	Sequence 1, Appl
38	39.6	2.7	16442	3	US-08-781-891-208	Sequence 208, App
39	39.2	2.7	1413	4	US-08-984-709A-52	Sequence 32, Appl
40	39.2	2.7	4403765	4	US-09-103-840A-2	Sequence 2, Appl
41	39.2	2.7	4411529	4	US-09-103-840A-1	Sequence 1, Appl
42	39.2	2.7	836	3	US-08-674-984-1	Sequence 1, Appl
43	39	2.7	836	5	PCR-US95-15601-1	Sequence 1, Appl
44	39	2.7	7791	2	US-08-149-097D-23	Sequence 23, Appl
45	39	2.7	7808	2	US-08-149-097D-22	Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-08-984-709A-49  
Sequence 49, Application US/08984709A  
Patent No. 6320032  
GENERAL INFORMATION:  
APPLICANT: Williams, Mark E.  
APPLICANT: Stauderman, Kenneth A.  
APPLICANT: Harpold, Michael M.  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, Suite 700  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,709A  
FILING DATE: 02-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 587-5360  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 249...7307  
OTHER INFORMATION:  
US-08-984-709A-49

Query Match 4.1%; Score 60; DB 4; Length 7898;  
Best Local Similarity 47.6%; Pred. No. 1.4e-05;  
Matches 277; Conservative 0; Mismatches 295; Indels 10; Gaps 3;

QY 531 CTTTCGGGACCTACTACTTGTACTACCTGGGAGAACCTATATGCCCTGGCAACCTGGTG 590  
DB 534 CTGCTGTGACACCCAGTGTGAGACACGACATGCTGTATATGCTCAACAGCGCGTG 593  
QY 591 TCCATTTGGTGTCCTGCTGCTGATGAGATGTCCTGCTGAGCGGTATGACTTC 650  
DB 594 ACCCTGGGATGTCGGGCTGTGAGAGCTGTAGTGGGCTCCGAGG---CTGCAAC 650  
QY 651 ATCTGGGGATTTCTCACTGCTCTTCAATGTACTACTGTGAGTGTGCTCTCAAG 710  
DB 651 ATCTGGAGGCTTTGAGCGCTTCAATTTCCGCTTTTGGCTGTGAGATGCTCAACAG 710  
QY 711 GTCTTGGCCCTGGGCTGCGAGGATACCTGTCTACCCAGAACGTGTTACGGGCTC 770  
DB 711 ATGTGGCTTGGGCTGTTCGGGAGAGTGTACTGTGGGTGACACGTGGAACAGGCTG 770  
QY 771 CTCACCTGTTCCTGCTGAGAGCCGAGATGATGGGCTGTGCTGTGGACATGAC 830  
DB 771 GATTTCTTCAATGCTGTGGCGGCG---ATGATGAGTACTGTTGGACGACACAGCTGAG 829  
QY 831 CCGATGCTGAACATGCTCAATGCTGTTCCTCTGCTATCAACCCAGCATGAAGCC 890  
DB 830 CCTCTGGCTATCAAGAGCCG-----TGCGGCTGCTGGGCGCCCTCCGCGCATCAACCG 883  
QY 891 GATGGCGTGGGCGCACTACCGTCTGGGCTGTGTCAGAACATGCTGGCTTGGGCG 950  
DB 884 CTTGCTTGCATGCGGATCTGTGCTACTGTGCTGTGATGACGCTGCCATGCTGGGAA 943  
QY 951 GATCCTGTGTGTGTACTACTACTATTTGCACTATTTGGATCACTGTTTAGAGCGT 1010  
DB 944 GCTCTTGTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1003  
QY 1011 CATTTGGCTTCTCTGGAACAGAGCTGGCCCTGCCAATGGCTGGGCGCTGTGG 1070  
DB 1004 GGTGGGCTCTCTGGGAACCCGCTGCTTCTCTGACAGCTCTTCTTCTTCTTCTTCT 1063  
QY 1071 GAGCTTGCAGAGCTGAGTACTGAGGCGCAACACTTGCATGA 1112  
DB 1064 GACCTTCTCTGGCGCTACTACTACAGAGGAGGCGCAGGA 1105

## RESULT 2

US-08-984-709A-51

Sequence 51, Application US/08984709A

Patent No. 6320032

GENERAL INFORMATION:

APPLICANT: Williams, Mark E.

APPLICANT: Stauderman, Kenneth A.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McCauliffe

STREET: 4250 Executive Square, Suite 700

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/984,709A

FILING DATE: 02-DEC-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 587-5360  
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 1669 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-984-709A-51

Query Match 3.5%; Score 51.4; DB 4; Length 1669;  
Best Local Similarity 47.5%; Pred. No. 0.0011;  
Matches 220; Conservative 0; Mismatches 236; Indels 7; Gaps 2;

QY 650 CATCTGGGAGATTCACATGCGCTTCTCAATGTGTACTACTCTGTGAGATTGCTGTCAA 709  
DB 22 CATCTGGAGGCTTTGACCGCTTCAATTTGCTTTTGGCGTGAAGATGTCATCAA 81  
QY 710 GGTCTTTGGCCCTGGGCTGCGAGGTTACCTGTCTTACCCAGAACGTGTTGACGGCT 769  
DB 82 GATGTGGCTTGGGCTGTTGCGGACAGAAAGTGTACTGCTGGGTGACAGCTGGAACAGCT 141  
QY 770 CCTCACCTGTTCCTGCTGAGAGCCGAGAGATGTTGGGCTGTCTGCTGTGGACATGA 829  
DB 142 GATTTCTTCAATGCTGTGGGCGGCGAT---GATGAGTACTGTTGGACGACACACGTA 200  
QY 830 CCGCATCTGAACATGCTCATGCTGTTCCTCTCTGCTGATATCCCAACAGATGAAC 889  
DB 201 GCTCTCGGCTATCAAGAGCCGTG-----CGGCTGTGCGGCGCTCCGCGCATCAAC 254  
QY 890 CGATGGCGTGTGGCGATACCGTCTGGGCTGTGTCAGAACATGAGTGGCTTGGCG 949  
DB 255 GGTGCTTGAAGTGGGATCTGTGCTACTGTCTGTGATACGCTGCCATGCTCGGGA 314  
QY 950 GATCCTGTGTGTGTACTACTACTATTTGCCATGATGGGATCACTGTTTAGAGCG 1009  
DB 315 AGTCTTCTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 374  
QY 1010 TCATTTGGCTTCTCTGGAACAGACAGCTGGCCCTGCCAATGGCTGGGCGCTGTG 1069  
DB 375 GGGCTGGCTCTCTGGGAACCGCTCTTCTTCTGACAGTGTCTTGTCTAGGAACACAC 434  
QY 1070 GAGCTTGCAGAGCTGAGTACTGAGGCGCAACACTTGCATGA 1112  
DB 435 TGACCTTCTCTGGCGCTACTACTACAGAGGAGGCGCAGGA 477

## RESULT 3

US-08-404-354B-1

Sequence 1, Application US/08404354B

Patent No. 5618720

GENERAL INFORMATION:

APPLICANT: Ellis, Steven Bradley

APPLICANT: Williams, Mark E.

APPLICANT: Harpold, Michael Miller

APPLICANT: Schwartz, Arnold

APPLICANT: Brenner, Robert

TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego



```

STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,354B
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53192
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79..5700
OTHER INFORMATION:
US-08-404-354B-1

Query Match 3.5%; Score 50.6; DB 1; Length 5975;
Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

QY 650 CATCTTGGGGAATTTCAACTGCGTCTTATATGTGTACTACCGCTGTGGAGTGGCTGCTCAA 709
DB 1464 CTTTCAAGACATCGCCCAATTCAGATGCTCTGTCTACACTTTCACCAATCGAATCTGTGAA 1523
QY 710 GGTCTTTGCCCCTGGGGCCGCGAGGGGTACTCTGCTACCCCAAGCAACGTTTGGAGGGCT 769
DB 1524 GATGTACGGGGCTGGGCCCTCGGCCCACTACTATGTCATCTTCAACCGCTTGGAGCTT 1583
QY 770 CCTACCGTGTCTCTGTGAGAGCCCGAGAGTGTGGGCTGCTGTGCGTGTGTGGACATGA 829
DB 1584 CGT----GGTGTGCGAGCCGACATCTCTGTGTGAGTGTGGGCGGCATGACGC 1639
QY 830 CCCGATCTGAACATGTCATCGTGTCCGCTTCTGCTGATTCATCCACAGATGAAGC 889
DB 1640 CGCTGGGCAATCTCCGTGTGGCGCTGCTGATCCGCTCTCTGAGGCTCTTCAAGATCACCAGT 1699
QY 890 CGATGGCCGTGGTGGCCAGTACCGCTCTGGGGCTGGTGGCAGACATGCTGGCTTGGGCG 949
DB 1700 ACTGAGCTGCGTCAAGCAACGTGGGCGCTCCCTGCTCAATCCATCCGCTCATGCGCT 1759
QY 950 GGATCTGTGTGTGGTCTACTACGATATTGGCATCATTTG 988
DB 1760 CGCTGCTGCTGCTGCTTCTTCTTCATCATCATCTTGG 1798

RESULT 4
US-08-314-083B-1
; Sequence 1, Application US/08314083B
; Patent No. 5686241

```

```

GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
CITY: 1660 Union Street
STREET: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,083B
FILING DATE: 28-SEPT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79..5700
OTHER INFORMATION:
US-08-314-083B-1

Query Match 3.5%, Score 50.6, DB 1, Length 5975.
Best Local Similarity 49.0%, Pred. No. 0.0027.
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1.

1:
650 CATCTGGGGATTCTTCACACTGCGCTTTCATATGTACTACCTGTTGAGATTGCTGCTCAA 709
Db 1464 CTTCGAAACATCGCCCAATCGAGTCTGCTGTCACCTTCCACCAATCGAGATGCTGTGA 1523
QY 710 GATCTTTCCCTGGGGCTCGGAGGGGTACTGTCTACCCACGACCAACGTTTGACGGGCT 769
Db 1524 GATGTCAGGGGCTGGGGCTCGGCCGACATGACTTAAATGTCATCTTCAACCGCTTGACATGCTT 1583
QY 770 CCTCACCGTTGCTGCTGAGAGCCGGAGAGATGTTGGGCTGCTGTCGCTGTGGAGATGA 829
Db 1584 GGT---GATGTCAGCGGCAATCTGAGACTCTGCTGTGGAGTGGGGCGCCATGACGC 1639
QY 830 CCCGATGCTGAACATGTCATCATGTTCCGGTCTCTGCTGATACATCCACAGATGAACG 889
Db 1640 CGCTGGGCAATCCGCTGTTGCCCTGCATCCGCTCTTGAGGCTCTTCAAGATACCAAGT 1699
QY 890 CGATGGCCGTGGTGGCCACTACCGTCTCTGGGGCTGGTGCAGAAACATGCGTGGCTTGGCG 949

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Db 1464 CTTGCAAGACACTGGCAATCGAGTGTGCTGTCTACTCTTACCAACGAGATGCTGTGAA 1523
QY 710 GGTCTTTGGCCCTGGGCTGCGAGGTAAGTCTGCTTACCCAGCAAGCTTTGAGGGCT 769
Db 1524 GATGTACGGGGGCGGCGCGGAGTATTCATGTCCATCTTCAACCGGCTTGACGCTT 1583
QY 770 CCTCACCGTTGCTGCTGGAGCGGAGATGATGGGCGCTGCTGCTGTGGAGACATGA 829
Db 1584 CGT----GGTGTGACAGCGGCACTCTGAGCTGCTGTGTGAGATGCGGCGCATACGC 1639
QY 830 CCGGATGCTGTAACATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
Db 1640 CGCTGGGCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1699
QY 890 CGATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
Db 1700 ACTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1759
QY 950 GGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 988
Db 1760 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1798

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## RESULT 7

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US-08-884-599-1
; Sequence 1, Application us/08884599
; Patent No. 6013474

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## GENERAL INFORMATION:

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; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: 'CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,599
; FILING DATE: 27-JUNE-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/314,083
; FILING DATE: 28-SEPT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53191B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 79...5700
; OTHER INFORMATION:
; US-08-884-599-1

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Query Match 3.5%; Score 50.6; DB 3; Length 5975;
Best Local Similarity 49.0%; Pred. No. 0.0027;
Matches 166; Conservative 0; Mismatches 169; Indels 4; Gaps 1;

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QY 650 CATCTGGGGATTCCTCACTGCTCTTCATTTGTACTACCTGTTGAGTGTGCTGCA 709
Db 1464 CTTGCAAGACATGCGCAATCGAGTGTGCTGTCTGCTTACCATGAGATGCTGTGAA 1523
QY 710 GGTCTTTGGCCCTGGGCTGCGAGGTAAGTCTGCTTACCCAGCAAGCTTTGAGGGCT 769
Db 1524 GATGTACGGGGGCGGCGCGGAGTATTCATGTCCATCTTCAACCGGCTTGACGCTT 1583
QY 770 CCTCACCGTTGCTGCTGGAGCGGAGATGATGGGCGCTGCTGCTGTGGAGACATGA 829
Db 1584 CGT----GGTGTGACAGCGGCACTCTGAGCTGCTGTGTGAGATGCGGCGCATACGC 1639
QY 830 CCGGATGCTGTAACATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
Db 1640 CGCTGGGCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1699
QY 890 CGATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
Db 1700 ACTGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1759
QY 950 GGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 988
Db 1760 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1798

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## RESULT 8

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US-09-404-650-1
; Sequence 1, Application us/09404650
; Patent No. 6309858

```

## GENERAL INFORMATION:

```

; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
; US-09-404-650-1

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Query Match 3.4%; Score 49.2; DB 4; Length 6816;
Best Local Similarity 47.5%; Pred. No. 0.0064;
Matches 217; Conservative 0; Mismatches 230; Indels 10; Gaps 2;

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QY 538 GCCACTACTACTTACTACTGCGGGAACCTCATGCGCTGCAACCTGGTGTCAATT 597
Db 421 GCACCCCGTGGTTGATGTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 598 GCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
Db 481 GCATGTACAGCCGCTGCGAGCAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 537
QY 658 GGATTCACACTGGCTCTTCACTTGTGTAACCTGTTGGAGATTGCTGCTCAAGGCTT 717

```



```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6048)
US-09-634-920-3
```

Query Match	3.1%;	Score 45.8;	DB 4;	Length 6048;
Best Local Similarity	51.7%;	Pred. No. 0.043;		
Matches 104;	Conservative 0;	Mismatches 97;	Indels 0;	Gaps 0;

QY	1077	CGAGCACTGGATCTAGCGGGCCAAACAATTCATGACTTTGGGGCTGGCCCTGGTCAACT	1133
Db	1035	CGAGAACCCCGACACAGGCTACCAACGCTTCGATTCCTTGCCCTGGGCCCTTCTTGCACT	1094
QY	1137	GTGGAACTTGATGGTGGTGAACAACATCGGAGGTTCTTCGATGCATATCGGCGCTACTC	1198
Db	1095	CTTCGCCGCTGATACGAGAGSACGCTGGGAGGGCCCTCTATCAGCAAGACCCTAGGTCCGC	1155
QY	1197	AGGCCCGTGGTCCAAAGATCTATTTTGTATTTGTGGTGCGTGTGTCGTGTCATCTGGGT	1256
Db	1155	AGGGAAGATCTACATGATGATCTCTTCATGCTGTGCATCTTCGGGGTCCCTCTACCTGGT	1214
QY	1257	CAACCTGTTCTCGGCCCTGAT	1277
Db	1215	GAACCTGATCTGGCCGTGGT	1235

RESULT 12  
US-09-404-650-12

GENERAL INFORMATION:  
APPLICANT: Dietrich, Paul S.  
APPLICANT: McGivern, Joseph G.  
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF  
TITLE OF INVENTION: AND USES  
FILE REFERENCE: R0043B-REG sequence listing  
CURRENT APPLICATION NUMBER: US/09/404,650  
CURRENT FILING DATE: 1999-09-23  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0

Query Match	3.1%	Score 45.8	DB 4	Length 6503
Best Local Similarity	47.9%	Pred. No. 0.044		
Matches 172; Conservative	0	Mismatches 177	Indels 10	Gaps 1

QY	650	CATCCTGGGGATTCTCAACAGCCTCTTTCATGTGTACTACCTGGTGGAGATCTCTCTAA	709
Db	2149	CATCTCGGGAATGTGCAAAATGTGTCTTTCACAGTATGTTTGGCCCTGGAGATATCTCTAA	2208
QY	710	GGTCTTTGCCCTTGGCCTTCGAGGGTACTGTCTTCAACCCAGCAACGTGTTTGGAGGGCT	769
Db	2209	ACGTGGCCGCTTTTGGGCTCTTTCACACTACTCTGGGAAACCTTCAACACATCTTTTGAGACGAT	2268
QY	770	CCTCACCGTGTCTCTGCTGAGAGCCGAGATGATGTGGGCTCGCTGTACGGTGTGGAGCATGA	829
Db	2269	CATCTGTATCATCATGAGATCTGTGGAAATCTGTGGGGCAGGCTGGACGGTGGCCCTGTCTG----	2322
QY	830	CCCCGATGCTGAACATGCTCATCTGTGTTCCGCTTCCTGCTATCATCCCAAGCATGAAGC	889
Db	2325	-----TGTGGCCCACTTCCGGTGTCTCGGGTGTCTGAAGCTGGTGGCTTCAAGCCGG	2378
QY	890	CGATGGCGCGTGGGGCCAGTAACCGTCTTGGGGCTGGTGAGAAACAATGGCTGGCTTTGGCG	949
Db	2379	CGCTGGGGGGCCACGCTCTGTGTGTCATATGAAGCAACATGACACAGGGCCACTTCTTCA	2438
QY	950	GGATTCCTGCTGTGTCTCACTACGATATTTGGCATATGGATGCAACTGTGTTTAGAGGC	1008

Db 2439 TGCTACCATGCTGTTCATCTTCATCTTCAGCATCTTGGGATGCATATCTTTGGCTGC 2493

RESULT 13  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Date of No. 5670367

1 GENERAL INFORMATION:  
2 APPLICANT: DORNER, F.  
3 APPLICANT: SCHEIFLINGER, F.  
4 APPLICANT: FALKNER, F. G.  
5 TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS  
6 NUMBER OF SEQUENCES: 52  
7 CORRESPONDENCE ADDRESS:

STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:

```

? PRIOR APPLICATION DATA: US/07/935,313
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE:
? APPLICATION NUMBER: 26-AUG-1991
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: pTZpc-F15
? FS-08-232-463-14

```

Query Match	3.1%;	Score 45.6;	DB 1;	Length 7218;
Best Local Similarity	5.9%;	Pred No. 0.051;		
Matches 21;	Conservative 188;	Mismatches 147;	Indels 0;	Gaps 0;

[illegible]

Qy	Db	Qy	Db
672	1267	732	1327
GTCTCANTGTGACACACCTGTGGATGCTCTCAAGCTCTTGGCCCTGGACCTGGA	YY	GGGACTGCTGTCACCCAGACAAACGTTTGACGGGCTCTCAACGCTGTCTCTGCT	YY
731	1326	787	1382
.....	.....	.....	.....

## RESULT 14

```

US-08-728-323A-1/c
Sequence 1, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yvan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein from Kaposi's
TITLE OF INVENTION: Saccoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3489
US-08-728-323A-1

```

Query Match	3.0%;	Score 43.8;	DB 2;	Length 3489;
Best Local Similarity	48.0%;	Pred. No. 0.11;		
Matches 155;	Conservative 0;	Mismatches 167;	Indels 1;	Gaps 1;

OY	TGCGTCATCAAGGTCTTTTGCCCTGGGACCTGGAGAGGTAACGTCCTACCCCACAACAGT	759
Dd	TTTCTCCTCATCTCTAACTCCTGCCTCGCTCCCTAACACCAGCTCCTGCTCCTCCTC	228
OY	TTGACGGGCTCTCACCGCTTCTCTGTGGAGGCCGAATGCTGGGCGCTGCTGTCGCG	819
Dd	TGCTCTCTCTCTCTCTGCTCTCTG-TTATCTCTGCTGTCTGTCTCATCTCTGCTG	222
OY	TTGGACATGACCCGATGCTGAACATGCTCATGCTGTCCGCTTCCGCTAFCATCCCC	879
Dd	CTGCTCATTCCTGCTGCTGCTCATCTCTCTCTGTGTATCCCTGGCTGGCTGCTGCTC	216

[illegible]

## RESULT 15

```

US-09-426-998-3
: Sequence 3, Application US/09426998
: Patent No. 6358706
: GENERAL INFORMATION:
: APPLICANT: DUBIN, ADRIENNE.E.
: APPLICANT: PIATT, JAYASHREE
: APPLICANT: ZHU, JESSICA Y
: APPLICANT: ERLANDER, MARK G
: APPLICANT: GALINDO, JOSE E
: TITLE OF INVENTION: DNA ENCODING HUMAN ALPHALG T-TYPE CALCIUM
: TITLE OF INVENTION: CHANNEL (ALPHALG-C)
: FILE REFERENCE: ORI-1057
: CURRENT APPLICATION NUMBER: US/09/426, 998
: CURRENT FILING DATE: 1999-10-26
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PATENTIN VER. 2.0
: SEQ ID NO 3
: LENGTH: 6822
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
US-09-426-998-3

```

Query Match	3.0%;	Score 43.8;	DB 4;	Length 6822;
Best Local Similarity	47.8%;	Pred. No. 0.14;		
Matches 164;	Conservative 0;	Mismatches 172;	Indels 7;	Gaps 1;

QY	651	ATCTGGGGGATTTTCACATCGTGCTTCATTGTGTACTACCTGTGGAGTGGTGGCTACAG	710
Db	346	ATCTCGAGAGGCGCTTTGATGACTTATCATCTTTGCTTTTCCGCTGAGATGGTGGTGAAG	405
QY	711	GTCTTTGCCCTGGGCTGCGAGGGTACTCTGTACCCAGACAGCTGTTTACGGCTC	770
Db	406	ATGGTGCGCTTGGGCAATCTTTGGGAAAATGTTTACTGGGAGACACTTGGAACGGGCTT	465
QY	771	CTCACCGTTTCTCGCTGAGAGGCGGAGATGATGGGCGCTGTGCTGCTGTGGGACATGAC	830
Db	466	GACTTTTTCATTCGTCATTCGGAG-----GGATGCTGGAGTACTCGTCTGACCTGGAGAA	518
QY	831	CCGATGCTGAACATGCTCATCGTGTCCGCTTCCTGCGTATCATATCCACGATGTAGGC	890
Db	519	CGTAGCTTTCACGCTGTACAGAGACAGTCCGTGGCTGTGCGACCGCTGATGAGGCCATTBACCG	578
QY	891	GATGGCCCTGTGGCCGACATACCGTCTCGGGGCTGAGTGACAGAACATCGTACGCTTTGGCGG	950
Db	579	GGTGGCCAGCATGTGGCATCTTGTACAGTGTGTGTGATACGCTCCATCTGTGGCAA	638
QY	951	GATCCTGGTGGTGTCTACACGATATTTGGCATATTTGGATC	993
Db	639	CGTCTGTGCTGTGCTTTCGCTTTCATCTTCATCTTCGGGATC	681

Search completed: October 8, 2002, 09:10:11  
Job time : 86 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 08:56:11 : Search time 59 Seconds  
(without alignments)  
913.064 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634  
Sequence: 1 MSSACWEATGRCRLGGMMV.....PGEDELTERLSOHPHLWLCR 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.032802.\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
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6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
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9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*  
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14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*  
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18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1671.5	63.5	22	AAM39017	Human polypeptide
2	1108	42.1	210	AAM24447	Human EST encoded
3	1020	38.7	192	AAW74828	Human secreted pro
4	922	35.0	333	AAB94563	Human protein sequ
5	784	29.8	591	AAU00502	Human TANO 437 pr
6	582.5	22.1	22	AAW40803	Human polypeptide
7	342	13.0	584	AAW67465	Amino acid sequenc
8	342	13.0	594	AAW75376	Human colon cancer
9	342	13.0	748	AAW60097	Human transport pr
10	342	13.0	816	AAW77820	Human ion channel
11	336	12.8	520	AAW23901	Rat Est encoded pr

12	208	7.9	395	22	AAM25607	Human protein sequ
13	195	7.4	2161	14	AAR33545	Sequence of the al
14	190	7.2	2161	16	AAR71001	Human neuronal cal
15	190	7.2	2161	16	AAR71002	Human neuronal cal
16	190	7.2	2161	19	AAW63137	Human calcium chan
17	190	7.2	2161	19	AAW63149	Human calcium chan
18	190	7.2	2161	21	AAW10568	Human calcium chan
19	189	7.2	724	13	AAR27648	Human CACNAIF sp1
20	189	7.2	1912	21	AAV49429	Human CACNAIF long
21	189	7.2	1977	21	AAV49430	Human neuronal cal
22	189	7.2	2270	16	AAR71010	Calcium channel al
23	189	7.2	2270	16	AAR69604	Human calcium chan
24	189	7.2	2270	21	AAW10582	Human T-type volta
25	187.5	7.1	2038	20	AAV14595	Human T-type volta
26	187.5	7.1	2044	20	AAV14594	Human T-type volta
27	187	7.1	2044	10	AAW95645	Rabbit skeletal mus
28	186.5	7.1	2251	16	AAR71009	Human neuronal cal
29	186.5	7.1	2251	16	AAR71081	Human calcium chan
30	186	7.1	175	22	AAW67469	Amino acid sequenc
31	186	7.1	1873	16	AAR73055	Rabbit skeletal ca
32	186	7.1	1873	18	AAW37711	Rabbit skeletal ca
33	186	7.1	1873	18	AAW18390	Rabbit skeletal ca
34	186	7.1	1873	21	AAV77544	Human neuronal cal
35	184	7.0	2138	16	AAR27607	Human calcium chan
36	184	7.0	2138	21	AAW10583	Calcium channel al
37	182	6.9	2338	21	AAW78900	Murine CACNAIF pro
38	180.5	6.9	1824	21	AAV49431	Human activated al
39	180	6.8	2034	20	AAW06300	Sequence of the al
40	178.5	6.8	1967	14	AAR33547	Human calcium chan
41	178.5	6.8	1968	19	AAW63139	Human neuronal cal
42	175.5	6.7	2237	16	AAR71006	Human calcium chan
43	175.5	6.7	2237	19	AAW63142	Human calcium chan
44	175.5	6.7	2237	21	AAW10573	Human calcium chan
45	175.5	6.7	2337	19	AAW37878	Human calcium chan

## ALIGNMENTS

RESULT 1	
1	AAM39017
ID	AAM39017 standard; Protein: 552 AA.
XX	
XX	AAM39017;
XX	22-OCT-2001 (first entry)
DE	Human polypeptide SEQ ID NO 2162.
XX	
XX	Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW	leukaemia.
XX	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US34263.
XX	
XX	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	

XX WPI: 2001-442253/47.  
DR N-PSDB; AA158173.  
XX

novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

PS Example 4; SEQ ID NO 2162; 10078pp; English.  
XX

the invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA136642-AA142213) with neurotrophic, immunosuppressant and cytoskeletal activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, C.N.S disorders, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and Note: The sequence data for this patent did not form part of the printed specification.

50 Sequence 552 AA;

Query Match	63.5%	Score 1671.5;	DB 22;	Length 552;
Best Local Similarity	68.1%	Pred. No. 9.3e-155;		
Matches 348;	Conservative 17;	Mismatches 73;	Indels 73;	Gaps 5

QY 48 QDDQDQDERITYQN.PESITSLVLTANNPDVIMPAYSKRAVAIFVTVIGSL 107  
:|||||  
Db 42 KDDQDQDERITYQN.PESITSLVLTANNPDVIMPAYSKRAVAIFVTVIGSL 101

QY 106 FLMNLLVLTISQPRGLMKSLSQTSFRRRLGTRAFELTSSMVEGGAQFOAIRRQSPST 167  
DB 102 FLMNLLVLTISQPRGLMKSLSQTSFRRRLGTRAFELTSSMVEGGAQFOAIRRQSPST 161  
QY 168 SLRRCRASSSSA-----TTTLTWGT-----SSPW 193

```
Db      162 LLOVLQAVQLDSSHKQAMMEKRVSYSLVLSAEFOKLFNELDRSVYNEHPPREYSQSF 221
          :
          :
97      194 QTWCPFACSWC-----MOMCILSVMTS-----WGFSTASLCTTC 231
```

DB 222 LQSAQFLFGHYEDYLGSLIALNLVSGFLVDADYLPAERDFELGLNCFEYYL 281  
KY 232 WSCSRSLPMACGECTCTPATCLTG-----SSPLSCWREMYGLSLM 274

Db 282 LEMILKYPALGKRGYSIYPSPNFDGLLVLLVLEISTLAYRLEPHDGMREMGILSLW 341  
275 DMTMLNMLVYFRRLIIPSMKPMAYASTVLGIYONNRAEGILLVYVYFAIGINLE 334

342 DMTMLNMLIVFRRLIPSMKPMAYASTVLGLVQNRAFGILLVYVYFAALIGNLE 401

335 RGIVTALPGSSSLAPANGAPCGSEFOLEYWANNEDFAALVTLMNLMVNNMQYFELDA 394

402 RGVIVALLPGNSSILAPANGSAPGSEFQLEYWMANNDDFAALVTLNMLNMYNNMQVFLLA 461

395 YRRISGPMKITYVLMVLVSVAIWNLFPLALLENFLHKMPRSHLQPLAGTPEATYQWT 454

462 YRRISGFSKITYFLVLMWLVSVIWNFLALILENF LHKMPRSHQPLAGTEALYQNT 521  
455 VELLFRDILEEPGEDELTERLSQHPHLWICR 485

522 VELLFRDILEPEDELTERTLSQHPHLWLCR 552

RESULT 2  
AAM24447  
ID AAM24447 standard; Protein; 210 AA  
XX

AC AAM24447,  
 VV

DT	12-OCT-2001	(first entry)
XY		

Human EST encoded protein SEQ ID NO: 1972

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse  
tomato; monkey; dog; sea urchin; expressed sequence tag; rcm.

KW **bi** diagnostics; **di** forensic test; **gen** gene mapping; **genetic** disorder; **div** biodiversity; **gene** therapy; **nut** nutrition.

**Homo sapiens.**

PN WO200154477-A2  
XX

PD 02-AUG-2001.  
XX

PE 25-JAN-2001; 2001WO-US02687.  
XX

FR 23-JAN-2000; 2000US-0491404  
PR 17-JUL-2000; 2000US-0617746

PR 15-SEP-2000; 2000US-0663870.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V.

XX WDT : 2001-12-14 14:51

DR N-PSDB; AAH99106.  
XX

Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -

Claim 20; Page 1256; 1275pp; English.

The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.

Sequence 210 AA;

Query Match	42.18;	Score 1108;	DB 22;	Length 210;
Best Local Similarity	99.58;	Pred. No. 3.7e-100;		
Matches 209; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

276 MTRRLNMLIVFRELRITPSMKPMAYVASTVLGVONMRAFGILVWVYVFAIGINLFR 335  
|||||  
1 MTRRLNMLIVFRELRITPSMKPMAYVASTVLGVONMRAFGILVWVYVFAIGINLFR 60

336 GVIALPGNSLAPANGSAPCGSEFQLEIYWANNEFDFAALVTLMLNLVYNNMOVFLDAY 395KY  
|||||  
61 GVIALPGNSLAPANGSAPCGSEFQLEIYWANNEFDFAALVTLMLNLVYNNMOVFLDAY 120b  
|||||

396 RRYSGPMSKITYEVLMMVSSVITWNLFTALLLENFLHKWDRSHLOPLAGPEATYQMTV 455Y  
121 RRYSGPMSKITYEVLMMVSSVITWNLFTALLLENFLHKWDRSHLOPLAGPEATYQMTV 180b

456 ELFRDILEEPGEDELTERTLSQPHIMLCR 485  
|||||  
181 ELFRDILEEPGEDELTERTLSQPHIMLCR 210



RESULT 3  
AAW74828  
ID AAW74828 standard; Protein: 192 AA.  
XX  
AC AAW74828;  
XX  
DT 25-JAN-1999 (first entry)  
XX  
DE Human secreted protein encoded by gene 100 clone H10AB52.  
XX  
KM Human; secreted protein; testis; tumour; foetal brain tissue;  
KM fusion protein; cancer; central nervous system; seizure;  
KM diagnosis; neurodegenerative disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 192  
FT label= unknown  
XX  
PD W09839448-A2.  
XX  
PE 11-SEP-1998.  
XX  
PE 06-MAR-1998; 98WO-US04493.  
XX  
XX 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043314.  
PR 11-APR-1997; 97US-0043568.  
PR 11-APR-1997; 97US-0043569.  
PR 11-APR-1997; 97US-0043576.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043669.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0044500.  
PR 23-MAY-1997; 97US-0044501.  
PR 23-MAY-1997; 97US-0044502.  
PR 23-MAY-1997; 97US-0044503.  
PR 23-MAY-1997; 97US-0044581.  
PR 23-MAY-1997; 97US-0044582.  
PR 23-MAY-1997; 97US-0044583.  
PR 23-MAY-1997; 97US-0044584.  
PR 23-MAY-1997; 97US-0044585.  
PR 23-MAY-1997; 97US-0044586.  
PR 23-MAY-1997; 97US-0044587.  
PR 23-MAY-1997; 97US-0044588.  
PR 23-MAY-1997; 97US-0044589.  
PR 23-MAY-1997; 97US-0044590.  
PR 23-MAY-1997; 97US-0044592.  
PR 23-MAY-1997; 97US-0044593.  
PR 23-MAY-1997; 97US-0044594.  
PR 23-MAY-1997; 97US-0044595.  
PR 23-MAY-1997; 97US-0044596.  
PR 23-MAY-1997; 97US-0044597.  
PR 23-MAY-1997; 97US-0044598.  
PR 23-MAY-1997; 97US-0044599.

PR 23-MAY-1997; 97US-0044600.  
PR 23-MAY-1997; 97US-0044601.  
PR 23-MAY-1997; 97US-0044612.  
PR 23-MAY-1997; 97US-0044613.  
PR 23-MAY-1997; 97US-0044614.  
PR 23-MAY-1997; 97US-0044615.  
PR 23-MAY-1997; 97US-0044616.  
PR 23-MAY-1997; 97US-0044617.  
PR 23-MAY-1997; 97US-0044618.  
PR 23-MAY-1997; 97US-0044633.  
PR 23-MAY-1997; 97US-0044633.  
PR 06-JUN-1997; 97US-0048964.  
PR 06-JUN-1997; 97US-0048974.  
PR 13-JUN-1997; 97US-0049610.  
PR 08-JUL-1997; 97US-0051926.  
PR 16-JUL-1997; 97US-0052874.  
PR 18-AUG-1997; 97US-0055724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056862.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.  
PR 22-AUG-1997; 97US-0056874.  
PR 22-AUG-1997; 97US-0056875.  
PR 22-AUG-1997; 97US-0056876.  
PR 22-AUG-1997; 97US-0056877.  
PR 22-AUG-1997; 97US-0056878.  
PR 22-AUG-1997; 97US-0056879.  
PR 22-AUG-1997; 97US-0056880.  
PR 22-AUG-1997; 97US-0056881.  
PR 22-AUG-1997; 97US-0056882.  
PR 22-AUG-1997; 97US-0056884.  
PR 22-AUG-1997; 97US-0056886.  
PR 22-AUG-1997; 97US-0056887.  
PR 22-AUG-1997; 97US-0056888.  
PR 22-AUG-1997; 97US-0056889.  
PR 22-AUG-1997; 97US-0056892.  
PR 22-AUG-1997; 97US-0056893.  
PR 22-AUG-1997; 97US-0056894.  
PR 22-AUG-1997; 97US-0056903.  
PR 22-AUG-1997; 97US-0056908.  
PR 22-AUG-1997; 97US-0056909.  
PR 22-AUG-1997; 97US-0056910.  
PR 22-AUG-1997; 97US-0056911.  
PR 05-SEP-1997; 97US-0057650.  
PR 05-SEP-1997; 97US-0057659.  
PR 05-SEP-1997; 97US-0057761.  
PR 12-SEP-1997; 97US-0058785.  
  
(HUMA-) HUMAN GENOME SCI INC.  
XX  
PA Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
XX Feng P, Ferris AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
XX Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
XX Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
XX WPI; 1998-506364/43.  
XX N-PSDB; AAV59610.  
XX  
DR New isolated human genes and the secreted polypeptide(s) they encode  
XX - useful for diagnosis and treatment of e.g. cancers, neurological  
XX disorders, immune diseases, inflammation or blood disorders  
XX  
PS Claim 1; Page 601-602; 721pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the nucleic  
XX acid molecule designated Gene 100 from the human cDNA clone H10AB52  
XX (deposited as clone ATCC 97901 and ATCC 209047).

CC The gene can be used to generate fusion proteins by linking to the gene  
 CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the  
 CC stability of the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC polypeptides in a sample or by determining the amount of the new  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses).

SO Sequence 192 AA:

Query Match 38.7%; Score 1020; DB 19; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-91;

Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 MKPAAVAVSVTLGVQNMRAFGGLVYVYFAITGINLRGVVALPGNSLAPANGSA 354  
 DB 1 MKPAAVAVSVTLGVQNMRAFGGLVYVYFAITGINLRGVVALPGNSLAPANGSA 60  
 QY 355 PCGSFDELEYMANNFDEFAALVTLNMLVYNNMQLADYRRYSGPMSKTYFLMWLVS 414  
 DB 61 PCGSFDELEYMANNFDEFAALVTLNMLVYNNMQLADYRRYSGPMSKTYFLMWLVS 120  
 QY 415 SVIWNLFLLALLENFLHKWDPKSHLOPLAGTPEATYQMTVELLFRDILEPGEDELTER 474  
 DB 121 SVIWNLFLLALLENFLHKWDPKSHLOPLAGTPEATYQMTVELLFRDILEPGEDELTER 180  
 QY 475 LSOHPHLMCR 485  
 DB 181 LSOHPHLMCR 191

#### RESULT 4

AAB94563 ID AAB94563 standard; Protein; 333 AA.

AC AAB94563;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:15339.

KW Human; primer: detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isega T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

PI WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

XX Claim 8; SEQ ID 15339; 2537pp + CD ROM; English.

PS The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dt primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC oligonucleotide which comprises a 3'-end sequence, where the  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

SO Sequence 333 AA:

Query Match 35.0%; Score 922; DB 22; Length 333;  
 Best Local Similarity 51.0%; Pred. No. 1.1e-81;

Matches 211; Conservative 20; Mismatches 64; Indels 114; Gaps 9;

QY 82 DVMIPTAKRRAYAFIFVFTVIGSLFLMNLTLTAIISOPRGYLMKSLQSLPFRRLGR 141

DB 34 EWMIPATSKNRAYAFIFVFTVIGSLFLMNLTLTAIISOPRGYLMKSLQSLPFRRLGR 93

QY 142 AAEFVSSNMGEGAPFOATRRGPSTSLRCRAPSSSATTTLTWTGSSPWTWCPFAC 201

DB 94 AAEFVSSNMGEGAPFOAVGVKPNLLQVLQKQDSSHKQ----- 135

QY 202 SWCMQWMCCLLSYWTSSWGSSTASSLCTTCMSSCSRSLPACGCTCPATCLTGSSPLS 261

DB 136 -----AMMEEVRSIGSV----- 147

QY 262 CWRPENYGLSLMDMTMLNLIVFRLRIIPSKPAAVAVSVTLGVQNMRAFGGLIYV 321

DB 148 -----LLSABEFQLFNL-----DRSVKHEHPREPRQSPFLQSAQFL--FG----- 188

QY 322 VYVFAIITGINFR-----GVYALPGNSSLAPANGSAPCGSFDELEYMANNFDDFAAL 376

DB 189 -HYFDYLG-NLIALANLVSICFVLADADYPAER-----DDF----- 225

QY 377 VTLMNLVNNMQLVFLDAYRYSGPMSKTYFLMWLVSSVIVNLFLLALLENFLHKWDP 436

DB 226 -ILMNLVNNMQLVFLDAYRYSGPMSKTYFLMWLVSSVIVNLFLLALLENFLHKWDP 284

QY 437 RSHLQPLAGTPEATYQMTVELLFRDILEPGEDELTERLSQHPHLMCR 485

DB 285 RSHLQPLAGTPEATYQMTVELLFRDILEPGEDELTERLSQHPHLMCR 333

#### RESULT 5

AA000502 ID AA000502 standard; Protein; 591 AA.

AC AA000502;

DT 18-JUL-2001 (first entry)

DE Human TANGO 437 protein.

KW Human; TANGO 315; clone jtdla045b02; TANGO 330; TANGO 437; TANGO 480;

KW cellular process regulator; gene therapy; mixed lymphocyte reaction;



QY 181 -TTTTLTWGT-----SSPWQTCWCPACSWCW----- 205  
 Db 379 MMEKRSYGSVLLSAEEFQKLFNEIDRSYKHPREXPQSPFLQSAQFLGHYYFDYIG 438  
 QY 206 -----MOMCCLLSVMTSS-----WGSTASSLCTTWCSCCSLFPACGCTCP 248  
 Db 439 NLIALANLVISICVFLVDADVLPARDPDLILGILNCVFIVYLLLEMLKVFALGIRGYLS 498  
 QY 249 TPATCTLGT-----SSPLSCRPPEMVGILSLMDMTMLNMLIVFRPLRI 291  
 Db 499 YPSVVFEGLLTVLVLLVEISTLAVYRLPHGKRPPEMVGILSLMDMTMLNMLIVFRPLRI 558  
 QY 292 IPSKPMVAVASTVGLVQNMRAAFGILV 320  
 Db 559 IPSKPMVAVASTVGLVQNMRAAFGILV 587

RESULT 6  
 AAM40803  
 ID AAM40803 standard; Protein; 321 AA.  
 AC AAM40803;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 5734.  
 XX  
 KW Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Dirmnac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI59959.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 2; SEQ ID NO 5734; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 CC  
 SQ Sequence 321 AA;  
 Query Match 22.1%; Score 582.5; DB 22; Length 321;  
 Best Local Similarity 46.6%; Pred. No. 1.9e-48;  
 Matches 151; Conservative 17; Mismatches 73; Indels 83; Gaps 7;  
 QY 63 NPESTLSIVLITANNPDVIRAYSKNRATFFTYVIGSLFIMNLITATITYSQFR 122  
 Db 3 NSPESTLSIVLITANNLFWLIPAYSKNRATFFTYVIGSLFIMNLITATITYSQFR 62  
 QY 123 GYLKSLQTSLEFRRRLGTRAAFEVLSMWGEGAFPOATRGRPSTSLFCRAPSSSA-- 180  
 Db 63 GYLKSLQTSLEFRRRLGTRAAFEVLSMWGEGAFPOATRGRPSTSLFCRAPSSSA-- 122  
 QY 181 -TTTTLTWGT-----SSPWQTCWCPACSWCW--- 205  
 Db 123 QAMMEKRSYGSVLLSAEEFQKLFNEIDRSYKHPREXPQSPFLQSAQFLGHYYFDY 182  
 QY 206 -----MOMCCLLSVMTSS-----WGSTASSLCTTWCSCCSLFPACGCT 246  
 Db 183 LGNLIALANLVISICVFLVDADVLPARDPDLILGILNCVFIVYLLLEMLKVFALGIRGY 242  
 QY 247 CPTPATCTLGT-----SSPLSC-----WRPEMVGILSLMDMTMLNMLI 284  
 Db 243 LSPSNVFDGLITVVLVLEISTLCTDCHNQAGGRBWR-----LLSLMDMTMLNMLI 297  
 QY 285 VFRFLRIIPSKPMVAVASTVGL 308  
 Db 298 VFRFLRIIPSKPMVAVASTVGL 321

RESULT 7  
 AAB67465  
 ID AAB67465 standard; Protein; 584 AA.  
 AC AAB67465;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Amino acid sequence of a calcium channel transport polypeptide.  
 XX  
 KW Calcium channel transport polypeptide; calcium trafficking;  
 KW neural disorder; HIV-induced dementia; immune system disorder;  
 KW rheumatoid arthritis; muscular disorder; muscle contractile dysfunction;  
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
 KW cardiovascular disorder; arrhythmia; renal disorder;  
 KW proliferative disorder; cancer; lung carcinoma; breast cancer.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200108635-A2.  
 PD 08-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-US20392.  
 XX  
 PR 28-JUL-1999; 99US-0145958.  
 PR 18-AUG-1999; 99US-0149446.  
 PR 14-MAR-2000; 2000US-0189064.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruden SM, Ni J, Shi Y;

XX WPI: 2001-138604/14.  
 DR N-PSDB; AAF55042.  
 XX  
 PT New isolated nucleic acid useful for diagnosis, detecting, or treating  
 PT or preventing diseases associated with anomalies in calcium trafficking  
 PT across the plasma membrane -  
 XX  
 PS Claim 11; Page 256-257; 259pp; English.  
 XX  
 CC The present sequence represents a calcium channel transport polypeptide.  
 CC The polynucleotides, polypeptides, and antibodies are useful for  
 CC preventing, treating, or ameliorating diseases associated with anomalies  
 CC in calcium trafficking across the plasma membrane. They are used to  
 CC diagnose, detect and treat or prevent diseases or conditions such as  
 CC neural disorders (e.g. HIV-induced dementia), immune system disorders  
 CC (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile  
 CC dysfunction), reproductive disorders, gastrointestinal disorders,  
 CC pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal  
 CC disorders, proliferative disorders, and/or cancerous diseases and  
 CC conditions (e.g. lung carcinoma or breast cancer).  
 XX  
 SQ Sequence 584 AA;  
 Query Match 13.0%; Score 342; DB 22; Length 584;  
 Best Local Similarity 25.4%; Pred. No. 1.5e-24;  
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;  
 QY 60 YFQNPESLTSILVLTANNPDVMIAPSKRAVAIFETVIGSLTLMNLTIAIIS 119  
 DB 30 YSTLENSTVSLFVLTANNPDVMPYSRNWSCVFETVISTELVIMNLTIAVVD 89  
 QY 130 QPRGYLMSIQTSLEFRRLGTRAAFEVLSSNVEGGAFOQATRGPGSTLRCRAPSSS 179  
 DB 90 TFNDIEKRKFKSLHKRAIQHAYRLISQRRPAG---ISYRQEGLMREPK-PRMSA 144  
 QY 180 ATTTLT-----TWGTSFQWQWCPACSCWMQMCCLL- 212  
 DB 145 RERYLTFKALNONNTPLSLKDPYDIYEVALKWKAKKREHW-----FDELPTALLI 198  
 QY 213 ---SVMTSSWGEFSTASSICTT---CW-----SCGSRSLPWACEGTCPPATCL 254  
 DB 199 FKGINILVSKAFQYFMIVLVAVNGWIIIVETFMKLGKGFESKHVPWSY-----LVFL 251  
 QY 255 T-----GSSPL-----SCWRP-----EMVGLSLMDMTMLNM-----LIYF 286  
 DB 252 TIYGELEFLKAVGLPVEYELSSGWNLFDSYVVFALGILAL-----ALNMEPEFIYVL 306  
 QY 287 R---FLRIIPSKPMAVAVASTYVLGVONKRAFGILVVVYVPAITIGINLFRGVIALPG 343  
 DB 307 RPLQILRLFKLERYRNVDITMFEELLPRMASLGLTLLIFYSFAIVGMEFFCGIYVPPNC 366  
 QY 344 NSSLAP-----ANGSAPCGSEFOLEYWANNPDDEAALVLTLMNLMVNNNOVFLD 393  
 DB 367 NISTYADAVRRNHTVGNRTV---VEEGYTLNNDNLNLSFVTLFELTVANNMYIME 422  
 QY 394 AYRRYSQWMSKITYFLVLMVLVSSVIVWNLFLALILENLEFLK 433  
 DB 423 GVTSGTSHMSRLYFMTFIVTMV-MTIIVATILEAFYVR 461  
 RESULT 8  
 AAG75376  
 ID AAG75376 standard; Protein: 594 AA.  
 AC AAG75376;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human colon cancer antigen protein SEQ ID NO:6140.  
 XX  
 KW Human: colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma.

XX OS Homo sapiens.  
 XX PN WO200122920-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000WO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 DR WPI: 2001-235357/24.  
 DR N-PSDB; AAH34781.  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 11; Page 7588-7590; 9803pp; English.  
 XX  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patient's own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB7789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 594 AA;  
 Query Match 13.0%; Score 342; DB 22; Length 594;  
 Best Local Similarity 25.4%; Pred. No. 1.5e-24;  
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;  
 QY 60 YFQNPESLTSILVLTANNPDVMIAPSKRAVAIFETVIGSLTLMNLTIAIIS 119  
 DB 40 YSTLENSTVSLFVLTANNPDVMPYSRNWSCVFETVISTELVIMNLTIAVVD 99  
 QY 120 QPRGYLMSIQTSLEFRRLGTRAAFEVLSSNVEGGAFOQATRGPGSTLRCRAPSSS 179  
 DB 100 TFNDIEKRKFKSLHKRAIQHAYRLISQRRPAG---ISYRQEGLMREPK-PRMSA 154  
 QY 180 ATTTLT-----TWGTSFQWQWCPACSCWMQMCCLL- 212  
 DB 155 RERYLTFKALNONNTPLSLKDPYDIYEVALKWKAKKREHW-----FDELPTALLI 208  
 QY 213 ---SVMTSSWGEFSTASSICTT---CW-----SCGSRSLPWACEGTCPPATCL 254  
 DB 209 FKGINILVSKAFQYFMIVLVAVNGWIIIVETFMKLGKGFESKHVPWSY-----LVFL 261  
 QY 255 T-----GSSPL-----SCWRP-----EMVGLSLMDMTMLNM-----LIYF 286  
 DB 262 TIYGELEFLKAVGLPVEYELSSGWNLFDSYVVFALGILAL-----ALNMEPEFIYVL 316  
 QY 287 R---FLRIIPSKPMAVAVASTYVLGVONKRAFGILVVVYVPAITIGINLFRGVIALPG 343  
 DB 317 RPLQILRLFKLERYRNVDITMFEELLPRMASLGLTLLIFYSFAIVGMEFFCGIYVPPNC 376



PN W0200164881-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US06530.  
 XX  
 PR 29-FEB-2000; 2000US-0185938.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAJ, Silos-santiago I;  
 XX  
 DR WPI: 2001-570694/64.  
 XX N-PSDB; AAH78802, AAH78803.  
 XX  
 PT Isolated ion channel polypeptide IC23927 useful in screening assays and  
 PT treatment of disorders, e.g., central nervous system disorders and pain  
 PT disorders  
 XX  
 PS Claim 14; Fig 1; 142pp; English.  
 XX  
 CC The present sequence represents the human ion channel 23927 (IC23927)  
 CC protein, which is claimed in the invention. The ion channel family of  
 CC proteins is a large family of membrane bound proteins responsible for a  
 CC wide range of transport and signalling functions in cells. The invention  
 CC comprises IC23927 proteins and nucleic acids. The IC23927 nucleic acids  
 CC and proteins may be used in screening assays, predictive medicine (e.g.,  
 CC diagnostic assays and pharmacogenetics) and treatment of disorders  
 CC characterised by insufficient production of IC23927 (e.g., central nervous  
 CC system disorders, pain disorders, or disorders of cellular growth,  
 CC differentiation or migration). The IC23927 nucleic acids and proteins are  
 CC also useful as targets for developing modulating agents to regulate a  
 CC variety of cellular processes, such as: ion transport (e.g., ion  
 CC conductance); membrane excitability and/or polarisation; synaptic  
 CC transduction (e.g., pain signalling); cell activation; muscle contraction;  
 CC cell growth; cell differentiation; cell migration and muscle contraction.  
 CC Administration of a modulator of IC23927 (especially by gene therapy) may  
 CC be used to treat pain or a pain disorder.  
 XX  
 SQ Sequence 816 AA;  
 Query Match 13.0%; Score 342; DB 22; Length 816;  
 Best Local Similarity 25.4%; Pred. No. 2.3e-24;  
 Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;  
 QY 60 YFONLPESLTSVLVLTANNPDVMPAYSKNRAVAIFVTVIGSLFTMLNLTATIS 119  
 DB 262 YFSTLENSIVSLFVLTANNPDVMPAYSKNRAVAIFVTVIGSLFTMLNLTATIS 321  
 QY 120 QFQGYLMKSLQTSIFRRRLGTTRAFAEVLSSMVBEGGAFPOATRGRGSTSLRFBPSSSS 179  
 DB 322 TFMDIEKRRKSKLLHRTAIOHAYRLISQRRPAG---ISYRQFGLMRFYK-PRMSA 376  
 QY 180 ATTTLT-----TWGTSPPQWTCOPFACSCMCMQMCCL- 212  
 DB 377 RERYLIFKALNQNTPLSLKDFYDIYEAALMKAKKNEHM-----FDELPRALLI 430  
 QY 213 ---SWTSSWGSTASSLCTT---CW-----SCCSRLPACBEGTPTPATCL 254  
 DB 431 FKGINILVSKAFQYFMYLVAANGVWILVETFMKGNFNSKHVPSY-----LVFL 483  
 QY 255 T-----GSSPL-----SCWRP-----EMVGLISLMDNRMNM-----LITF 286  
 DB 484 TIYGVLEFLKAVGLGVEYETISSGMNLPDSVTFAPFLGLAL-----ALMMEPFYFIVL 538  
 QY 287 R---FLRIIPSKPMAVVAIVGLVQNMRAFGILVVVVYFAIGINLFRGVIALPG 343  
 DB 539 RPIQLRLRFLKRRYRNVLDTMELPRMASLGLTILIFYSFAIYGMFPCIVPNC 598  
 QY 344 NSSLAP-----ANSAPGSGFQLEIYMANNFDDFAALVLTLMNVVNNMOVFD 393  
 DB 599 NTSTADAYRMRNHTVGNRTV---VEEGYYLNNFDNINLSHVTLELTVVNNMYIME 654

QY 394 AYRRYSGPWSKRIYFVLMMLVSSVIMVNLFLALILENFK 433  
 DB 655 GVTQSOTSHWSRLYFMFTFIVIMVW-MTIVAPLEAFVR 693  
 RESULT 11  
 ID AAM23901  
 XX AAM23901 standard; Protein; 520 AA.  
 AC AAM23901;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Rat EST encoded protein SEQ ID NO: 1426.  
 XX  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN W0200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US02687.  
 XX  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HXSE-) HXSEQ INC.  
 XX  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WPI: 2001-476164/51.  
 DR N-PSDB; AAH98560.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 20; Page 992-993; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention.  
 XX  
 SQ Sequence 520 AA;  
 Query Match 12.8%; Score 336; DB 22; Length 520;  
 Best Local Similarity 25.0%; Pred. No. 4.9e-24;  
 Matches 115; Conservative 72; Mismatches 159; Indels 114; Gaps 17;  
 QY 60 YFONLPESLTSVLVLTANNPDVMPAYSKNRAVAIFVTVIGSLFTMLNLTATIS 119  
 DB 30 YFSTLENSIVSLFVLTANNPDVMPAYSKNRAVAIFVTVIGSLFTMLNLTATIS 89  
 QY 120 QFQGYLMKSLQTSIFRRRLGTTRAFAEVLSSMVBEGGAFPOATRGRGSTSLRFBPSSSS 179  
 DB 90 TFMDIEKRRKSKLLHRTAIOHAYRLISQRRPAG---ISYRQFGLMRFYK-PRMSA 144  
 QY 180 ATTTLT-----TWGTSPPQWTCOPFACSCMCMQMCCL- 212  
 DB 145 RERYLIFKALNQNTPLSLKDFYDIYEAALMKAKKNEHWD-----ELPRALLI 198





DR N-PSDB; AA037811.

XX DNA encoding specific human calcium channel sub-units - used for  
 PT identifying calcium channel agonists and antagonists and  
 PT diagnosing Lambert Eaton syndrome

XX Disclosure: Page 93-101; 150pp; English.

XX The alpha 1D subunit cDNA was isolated using fragments of the  
 CC rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a  
 CC probe to screen a cDNA library of a human neuroblastoma cell line,  
 CC IMR32, to obtain clone alpha 1.36. This clone was used as a probe to  
 CC screen additional IMR32 cell cDNA libraries to obtain overlapping  
 CC clones which were then employed for screening until a sufficient  
 CC series of clones to span the length of the nucleotide sequence  
 CC encoding the human alpha 1D subunit were obtained, see AA037811.  
 CC AA037812 provides the sequence of an alternative exon encoding the 156  
 CC transmembrane domain of the alpha 1D subunit. The alpha 1D protein  
 CC has a calculated Mr of 245,163.

XX Sequence 2161 AA;

Query Match 7.4%; Score 195; DB 14; Length 2161;  
 Best Local Similarity 18.7%; Pred. No. 2.2e-09;  
 Matches 95; Conservative 80; Mismatches 157; Indels 176; Gaps 20;

```

QY 12 CRLGGMMVPTGWNVGLSLMGDPVPMSCRFCSQDDGDRERLTYFQNLPESTSL 71
DB 333 CR--SGWVAPNGI-----TNDNFAFAMLTIV 357
QY 72 LVLLTTANPDVMPAYSKNRAVA-----IFFIVTYIGSLFNLMLTAITYSQFGYLM 136
DB 358 FQCTIMEGMTDVL---YWNDAWGFELPWYFVSLVTFGSFVLNLVGLSGEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAAFEVLSSWVG-----EGG-----APF----- 158
DB 415 KAKARGDFQKLREKQLEEDLKGILDMITQAEIDIPNEEGEGEGEGRNTSMPTSETESV 474
QY 159 -----QATRRGPSTSLRCRAPSSSANTTTLTWGTSSPWOPTWCPACSWC----- 204
DB 475 NTEWVSGEENRGCCGSL--COAISKSK-----LSRRMRMRNFRNTRCRAAVKSV 523
QY 205 --WMOMCCCL-LSVMTSS-----WGF--STASSLCTTCWSC-----GSRSLP--- 240
DB 524 TFYWLIVLVLFNTLTISSEHYNOPDMLTQIDIANKVLALFTCEMLYKMSVLGQAYF 583
QY 241 -----WACEGTCPTPATCLTGSSPLSCWRPEWGLSLMDMTRLMLMLIVPRFLR 290
DB 584 VSLFNRFDCFVYCGITETILVELEIMSPLG-----ISVRCVRLLR 625
QY 291 IIPSMKPMAVVASTVLGVONMRAFGILVYV---YFAIIGINLFRGVIALPENGSSL 347
DB 626 IFKVTHTMTSLSLVSLMSKMSIASLLTLFLFTIFSLGMOFLGFKF----- 676
QY 348 APANGSAPGCFEQLRYMANNFDDFAALVLTMLNMLVNVNMO--VFIDAVRYSQPMK-- 404
DB 677 -----NFEDETQTKSTFDNFPQALLTVFQILITGEDMNAVMYDGINATGSSSGM 726
QY 405 ---LYFVLMVWVSVIWNLFLLIEN 429
DB 727 IVCITFIILFCGNITLLNVLAIADVN 754

```

RESULT 14

AA071001

AA071001; standard; Protein; 2161 AA.

30-NOV-1995 (first entry)

Human neuronal calcium channel subunit alpha 1D.

KW Calcium channel subunit; antagonist; agonist; diagnosis;

XX Lambert Eaton Syndrome.

XX Homo sapiens.

XX WO9504822-A.

XX 16-FEB-1995.

XX 11-AUG-1994; 94WO-US09230.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Ellis SB, Gillespie A, Harpold MW, McCue AF, Williams ME,

XX WPI; 1995-090900/12.

XX N-PSDB; AA084653.

XX DNA encoding human calcium channel sub-unit(s) - used for

XX developing prods. for studying calcium channels, e.g. for

XX obtaining agonists and antagonists

XX Disclosure: Page 116-126; 285pp; English.

The alpha 1D subunit cDNA has been isolated using fragments of the  
 CC rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a  
 CC probe to screen a cDNA library of human neuroblastoma cell line  
 CC IMR32, to obtain clone alpha 1.36. This clone was used as a probe to  
 CC screen additional IMR32 cell cDNA libraries to obtain overlapping  
 CC clones which were then employed for screening until a sufficient  
 CC series of clones to span the length of the nt sequence encoding the  
 CC human alpha 1D subunit was obtd. Full-length clones were then  
 CC constructed by ligating partial clones. AA084653 shows the nt sequence  
 CC of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has  
 CC a calculated Mr of 245,163. It contains four putative internal  
 CC repeated sequence regions which represent 24 putative transmembrane  
 CC segments. It mediates DHP-sensitive high-voltage, long-lasting  
 CC calcium channel activity.

XX Sequence 2161 AA;

Query Match 7.2%; Score 190; DB 16; Length 2161;  
 Best Local Similarity 18.5%; Pred. No. 6.7e-09;  
 Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

```

QY 12 CRLGGMMVPTGWNVGLSLMGDPVPMSCRFCSQDDGDRERLTYFQNLPESTSL 71
DB 333 CR--SGWVAPNGI-----TNDNFAFAMLTIV 357
QY 72 LVLLTTANPDVMPAYSKNRAVA-----IFFIVTYIGSLFNLMLTAITYSQFGYLM 136
DB 358 FQCTIMEGMTDVL---YWNDAWGFELPWYFVSLVTFGSFVLNLVGLSGEFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAAFEVLSSWVG-----EGG-----APF----- 158
DB 415 KAKARGDFQKLREKQLEEDLKGILDMITQAEIDIPNEEGEGEGEGRNTSMPTSETESV 474
QY 159 -----QATRRGPSTSLRCRAPSSSANTTTLTWGTSSPWOPTWCPF-----AC 201
DB 475 NTEWVSGEENRGCCGSL--COAISKSK-----LSRRMRMRNFRNTRCRAAVKSV 523
QY 202 SMCWOMCCCL-LSVMTSS-----WGF--STASSLCTTCWSC-----GSRSLP--- 240
DB 524 TFYWLIVLVLFNTLTISSEHYNOPDMLTQIDIANKVLALFTCEMLYKMSVLGQAYF 583
QY 241 -----WACEGTCPTPATCLTGSSPLSCWRPEWGLSLMDMTRLMLMLIVPRFLR 290
DB 584 VSLFNRFDCFVYCGITETILVELEIMSPLG-----ISVRCVRLLR 625
QY 291 IIPSMKPMAVVASTVLGVONMRAFGILVYV---YFAIIGINLFRGVIALPENGSSL 347

```

```

Db      626  IFKVTYRHTSISNLYVASLMSKMSIASILLFLFIIFISLGMQLFGKF----- 676
QY      348  APANGSAPCGSEFQLEYWANNFDEFAALVTLNMLNMYNNMO--VFDDARYRYSQPMK-- 404
Db      677  -----NFDETQTKRSTFDNFPOALLTVFQILTGEDMNAVMYDGIAYGSPSSGM 726
QY      405  ---TYFVLMVLVSVIWNLFALILEN 429
Db      727  IVCIYFIILFCGNYILLNVFLATAVDN 754

RESULT 15
AAR71002
ID      AAR71002 standard; Protein; 2161 AA.
XX      AAR71002;
XX      30-NOV-1995 (first entry)
DE      Human neuronal calcium channel subunit alpha 1D including alternative.
DE      exon encoding the 156 transmembrane domain.
XX      Calcium channel subunit; antagonist; agonist; diagnosis;
XX      Lambert Eaton Syndrome.
XX      Homo sapiens.
XX      Key Location/Qualifiers
XX      FH Misc-difference 373..406
XX      FT /label= encoded by alternative exon
XX      PN W09504822-A.
XX      PD 16-FEB-1995.
XX      PF 11-AUG-1994; 94WO-US09230.
XX      PR 11-AUG-1993; 93US-0105536.
XX      PR 05-NOV-1993; 93US-0149097.
XX      PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX      PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
XX      WPI; 1995-090900/12.
XX      DR N-PSDB; AA084654.
XX      PT DNA encoding human calcium channel sub-unit(s) - used for
XX      PT developing prods. for studying calcium channels, e.g. for
XX      PT obtaining agonists and antagonists
XX      PS Disclosure; Page 126-127; 285pp; English.
XX      CC The alpha 1D subunit cDNA has been isolated using fragments of the
XX      CC rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a
XX      CC probe to screen a cDNA library of human neuroblastoma cell line
XX      CC IMR32, to obtain a clone alpha1.36, This clone was used as a probe to
XX      CC screen additional IMR32 cell cDNA libraries to obtain overlapping the
XX      CC clones, which were then employed for screening until a sufficient
XX      CC series of clones to span the length of the nt sequence encoding the
XX      CC human alpha 1D subunit was obtained. Full-length clones were then
XX      CC constructed by ligating partial clones. AA084653 shows the nt sequence
XX      CC of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has
XX      CC a calculated Mr of 245,163. It contains four putative transmembrane
XX      CC repeated sequence regions which represent 24 putative transmembrane
XX      CC segments. It mediates DHP-sensitive high-voltage, long-lasting
XX      CC calcium channel activity. AA084654 shows an alternative exon encoding
XX      CC the 156 transmembrane domain. The difference occurs in AAs 373-
XX      CC 406.
XX      SQ Sequence 2161 AA;

```

```

Query Match      7.2%; Score 190; DB 16; Length 2161;
Best Local Similarity 18.5%; Pred. No. 6.7e-09;
Matches 94; Conservative 83; Mismatches 155; Indels 176; Gaps 20;

QY      12  CRLGGMWVPTGWRGRLSLGSGDGVVWSCRFSQDDGDRRLTYFQVLPSPSLSL 71
Db      333  CR--SGWVGPNGI-----TFEDFAFAMLTIV 357
QY      72  LVLLTANNPDVWIPAYSKNRAVA-----IFFIVTIGSLFLMLTLTAIISQFQYLM 126
Db      358  FQCTIMEGHTDL---YWNDAIGWEMPMVYFVSLIIISFFVIMLVGLSGERSKERE 414
QY      127  KSLQTSLFRRLRGTRAFAFVLSMWG-----EGG-----AP----- 158
Db      415  KAKARDDFQRLREKQOLEEDIKGLDWTQAEIDIPENEEGEGEKRTSMPTSETESV 474
QY      159  -----QATRRGPSTSLRCPAPSSSATTTLTWTGTSPPQWTCPF-----AC 201
Db      475  NTEVSGEGENRCCGSL--QAISSK-----LSRRRRNRNRRRCRAAVKSV 523
QY      202  SMCMMQMCCLLSVMTSS-----WGF---STASSLCTTCWSC-----CSRSLP--- 240
Db      524  TFYWLIVLVFLMVTIRLISSEHYNQPDWLQIQDIANKVLLALETCMLVKMYSLGIQAYF 583
QY      241  -----WACEGTCPTPATCTLTGSSPLSCWRPMWGLSLMDYTRMLNMLIVRFRLR 290
Db      584  VSLFRPDCFVCGIETILVELIEMSPLG-----ISVRCYRLLR 625
QY      291  IIPSMKPMAVASVVLGLVONMRAFGIIVVY---VFPAIIGINLFRGYVALPQNSSL 347
Db      626  IFKVTYRHTSISNLYVASLMSKMSIASILLFLFIIFISLGMQLFGKF----- 676
QY      348  APANGSAPCGSEFQLEYWANNFDEFAALVTLNMLNMYNNMO--VFDDARYRYSQPMK-- 404
Db      677  -----NFDETQTKRSTFDNFPOALLTVFQILTGEDMNAVMYDGIAYGSPSSGM 726
QY      405  ---TYFVLMVLVSVIWNLFALILEN 429
Db      727  IVCIYFIILFCGNYILLNVFLATAVDN 754

```

Search completed: October 8, 2002, 10:02:41  
 Job time : 62 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:02:16 ; Search time 24 Seconds

(without alignments)  
493.601 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634  
Sequence: 1 MSSACWEATGRCRLGGWVY.....PGEDELTERTLSQPHLWLCR 485

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents, AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/6CTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	192	7.3	1872	6	5386025-6
2	190	7.2	2161	1	US-07-745-206A-2
3	190	7.2	2161	1	US-08-455-543A-49
4	190	7.2	2161	1	US-08-455-543A-51
5	190	7.2	2161	2	US-08-223-305C-49
6	190	7.2	2161	2	US-08-223-305C-51
7	190	7.2	2161	2	US-08-311-363-2
8	189	7.2	1873	1	US-08-336-257A-7
9	186	7.1	1873	1	US-08-435-625B-4
10	185.5	7.0	1754	1	US-07-745-206A-13
11	185.5	7.0	1754	2	US-08-311-363-13
12	178.5	6.8	1968	2	US-08-455-543A-45
13	178.5	6.8	1968	2	US-08-223-305C-45
14	175.5	6.7	2237	1	US-08-455-543A-48
15	175.5	6.7	2237	2	US-08-223-305C-48
16	175.5	6.7	2237	4	US-09-268-163-8
17	175.5	6.7	2237	3	US-08-713-118-2
18	175.5	6.7	2237	4	US-09-452-007-2
19	175.5	6.7	2239	1	US-08-455-543A-47
20	175.5	6.7	2339	2	US-08-223-305C-47
21	175.5	6.7	2339	2	US-09-268-163-6
22	175.5	6.7	2343	4	US-09-268-163-4
23	174.5	6.6	823	1	US-07-745-206A-15
24	174.5	6.6	823	2	US-08-311-363-15
25	171	6.5	2273	4	US-09-426-998-5
26	170.5	6.5	1835	4	US-09-404-650-5
27	169.5	6.4	2353	4	US-08-984-709A-50

28	168.5	6.4	2265	2	US-08-149-097D-36	Sequence 36, Appl
29	168.5	6.4	2509	2	US-08-149-097D-35	Sequence 35, Appl
30	168	6.4	2336	4	US-09-268-163-10	Sequence 10, Appl
31	167.5	6.4	2175	4	US-09-404-650-2	Sequence 2, Appl
32	167.5	6.4	2188	4	US-09-404-650-4	Sequence 4, Appl
33	163.5	6.2	1956	4	US-08-843-417-10	Sequence 10, Appl
34	160.5	6.1	2104	2	US-08-808-793-4	Sequence 4, Appl
35	160.5	6.1	2104	3	US-08-772-512A-4	Sequence 4, Appl
36	160.5	6.1	2105	3	US-08-808-793-3	Sequence 3, Appl
37	160.5	6.1	2105	3	US-08-772-512A-3	Sequence 3, Appl
38	156	5.9	813	3	US-08-836-325-8	Sequence 8, Appl
39	155.5	5.9	1968	1	US-07-745-206A-7	Sequence 7, Appl
40	155.5	5.9	1968	2	US-08-311-363-7	Sequence 7, Appl
41	155.5	5.9	2516	3	US-08-895-590-2	Sequence 2, Appl
42	155.5	5.9	2516	4	US-09-634-920-4	Sequence 4, Appl
43	154.5	5.9	2016	4	US-08-836-325-10	Sequence 10, Appl
44	151.5	5.8	1984	3	US-08-836-325-10	Sequence 2, Appl
45	150.5	5.7	1011	3	US-08-836-325-2	

## ALIGNMENTS

RESULT 1  
5386025-6  
Patent No. 5386025  
; APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL  
; M. CAMPBELL, KEVIN P.  
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/482,384  
; FILING DATE: 20-FEB-1990  
; SEQ ID NO: 6  
; LENGTH: 1872  
5386025-6

Query Match 7.3%; Score 192; DB 6; Length 1872;  
Best Local Similarity 18.3%; Pred. No. 9.2e-10;

Matches 95; Conservative 81; Mismatches 165; Indels 178; Gaps 19;

QY	58	LTFFONLEPESLTSLLVLTITANPDVMIKAYSKNRYA-----IFETVYIGSLFMTL 112	
DB	272	ITHFNFQSMFTVYQCTIEGMDTVL--TYVDALIGNEMPIYFTLLILSGFLLNL 328	
QY	113	LTATTSQPRGLKMSLQTSFRRRLGTRAFEVLSSWVG----- 152	
DB	329	VLGVLISGEFTKEREKAKSGTFOKLEKQOLEEDLRGYMSWITOGEDYEDLREGKLSL 388	
QY	153	-EGAFPOATR--RQPTSLRFGRAPSSSATTLTWTGSSPMQTM---CPFACS--- 202	
DB	389	EEGSDTSLYEIEGLNKTIQFIR-----HKKNNRYFRMKCHDLVK 430	
QY	203	---WCMQMC-----CLLSVYT-----SSWGFSTAS 225	
DB	431	SRVFWLIVLILVALNTLSIAEHHNPLMLTHLODIANRVLLSFTLEMLKMGGLRQ 490	
QY	226	SLCT-----TQWSSCSRSLP--WAGEGTCPPRATGTLSSPLSCRPREMGILSLMDTRM 279	
DB	491	YFMSTFNRFDCFWVCSGLLELLVESGAMP---LGIYLRG----- 529	
QY	280	LNMILVERFLRIISMKPMAYVASTVLGLVQNMRAFGIIVVVY---YFAIGINLFRG 336	
DB	530	-----IRLRLFKITTKWTSLSLVLSLNSISLILLLFLFTITRALLGMLFGG 583	
QY	337	VIVALLPGNSLAPANGSAPCGSFQLEWANNPDFAALVTLNMLVNNW--QVFLDAY 395	
DB	584	RY-----DFEDTEVRSNENFPOALISYFOVLTGDMSSVMYNGI 624	
QY	396	RRYSGPWSK-----IFVLMMLVSSVIVMVDLFTALIENTLH-----TWDRSHL 440	
DB	625	MAYGSPSPGVLCVLYITITIIIFVCGNTIILNVFTLAIIVDNLAEASLTSQAKAAEKKRR 684	

QY 441 OPLAGPEATYMTVELLFRDILEEPGEDELTERLSQHP 479  
DB 685 KMSRGLPDKT-----EERKSVMAKKLEQRP 709

## RESULT 2

US-07-745-206A-2  
Sequence 2, Application US/07745206A  
Patent No. 5429921  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2161 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-2

Query Match 7.28; Score 190; DB 1; Length 2161;  
Best Local Similarity 18.58; Pred. No. 1.8e-09;  
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGMMVPTGWVRLGELSLMGDPVVPWSCRFCSQDGDODRRLTYFQNLPESLTSL 71  
DB 333 CR--SGWGRNGT-----TNDNRAFAMLIV 357  
QY 72 LVLLTANPDVMIPIAYSKNRAYA-----IFETVYVIGSLFLMLTALITTSQFRGYLM 126  
DB 358 FQCTMEGTVDL---YWMNDAMGFELPVWYFSLVIFGSEFVNLVLGVLSEFSKERE 414  
QY 127 KSLQTSLEFRLRLGTRAPEVLSNVG-----EGG-----AFP----- 158  
DB 415 KAKARGDQKREKQLEEDKGYLDMITQAEIDDPENEEGEGEGGRNTSMPTSESEV 474  
QY 159 -----QATRRGPSTSLRCRAPSSSATTTLTTWGTSSPMQWCP-----AC 201  
DB 475 NTEVNSGEGNRGGCGSL--CQALSKSK-----LSRRWRNRNFRNRRCRAAVKSV 523  
QY 202 SMCWQKQCL-LSVWTS-----WGF-----STASSLCTTCWGC-----CSNLP--- 240  
DB 524 TFYMLVIVLVLNLTLSSEHYNQPDMLTQIDIANRVLLALFTCEMLVKMYSGLQAYF 583  
QY 241 -----WACGTCTPTATCTLGSSPLSCWBPENVAGLLSLMDMTMLNMLIVFRLR 290

DB 584 VSLFNRDPCFVCGGITEITLVELEINSPUG-----ISVRCVRLR 625  
QY 291 IIPSMKPAVAVSTVLGLVONMRAFGLVVVY---YFALIGINLFGVYVALPQNSSL 347  
DB 626 IFKTRWTSLSNIVASLNSMKSIAASLILLLFLFIIFSLDMQLEFGKF----- 676  
QY 348 APANGSAPCGSFEQLEYWANNFDEFAALVTLNMLNMYVNNWQ-VFLDARYRSGPSK-- 404  
DB 677 -----NFDETQTKRSTFDFNFPQALLTVFOILTGEDMNAVMYDGINAYGSPSSGM 726  
QY 405 ---YFVIMLVSSVIVWNLFLALLEN 429  
DB 727 IVCYIFILFCGNFILLNVLALAVDN 754

## RESULT 3

US-08-455-543A-49  
Sequence 49, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2161 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-49

Query Match 7.2%; Score 190; DB 1; Length 2161;  
 Best Local Similarity 18.5%; Pred. No. 1.8e-09;  
 Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

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QY 12 CRLGGWVPTGWRGELSLMGDPVWSCRFCSDQDDGDRRLTYFQNLPESTLSL 71
DB 333 CR--SGWVGPNCGI-----TNDNFAPFAMLTIV 357
QY 72 LVLLTANPDVMIPTAYSKNRAYA-----IFFTVTVIGSLFLMNLTLTIYSQFGYLM 126
DB 358 FOCITMEGTDLV---YWNDAIGWEPWYFVSLIIGSFVLNLVGLSGEFSKERE 414
QY 127 KSLQTSLFRRLGTAAFEVLSSWVG-----EGG-----APP----- 158
DB 415 KAKARGDFQKLRKQOLEEDLKGIDWITQAEIDPENEEGEGEGRKNTSMPTSESV 474
QY 159 -----QATRRGPSTSLRCPAPSSSATTTLTWTGSSPWOTWCF-----AC 201
DB 475 NTENVSGEGENRCCGSL--COAISKSK-----LSRRWRMRNRRRCRAAVKSV 523
QY 202 SMCWMOMCL--LSVMTSS-----WGF-----STASSLCTTQMSC-----CGRSLP--- 240
DB 524 TTYMLVIVLFTLITISSEHYNQDPWLQIODIANKVLALFTCEMLYKMSLGLQAYF 583
QY 241 -----WACEGTCPATCLTGSSPLSCWRPEMVGLLSLMDTRMLNLIVRFLR 290
DB 584 VSLFNRDFCVVCGGITETILVLELMSPLG-----ISVRCRLLLR 625
QY 291 TTPSKPMVAVSTYGLVQNNRARGGILVYV---YPAIIGINLFRGYVALPQNSSL 347
DB 626 IFRVTRHMTSLSNLVAFLNSMKMSIASLLILFLIIFSLGMQIFGKRF----- 676
QY 348 APANSGAPCGFEQLEYMANNFDDFAALVTLMNLVNVNMQ--VFIDATRRRSQPSK-- 404
DB 677 -----NFEDETQTKRSTFDPNFPQALTYFQILGEDMNAVMTDGIMAYGGPSSGM 726
QY 405 ---IYFVLMVLVSVIWNMLFALILEN 429
DB 727 IVCITPILIFIGNYIILLNVFLAIANDN 754

```

RESULT 4  
 US-08-455-543A-51  
 Sequence 51, Application US/08455543A  
 Patent No. 5792846  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA

```

/ ZIP: 92101-2926
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/455,543A
/ FILING DATE: May 31, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/223,305
/ FILING DATE: April 4, 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/868,354
/ FILING DATE: April 10, 1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/745,206
/ FILING DATE: 15-AUG-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/620,250
/ FILING DATE: 30-NOV-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/482,384
/ FILING DATE: 20-FEB-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/603,751
/ FILING DATE: 04-APR-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: NO PCT/US89/01408
/ FILING DATE: 04-APR-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/176,899
/ FILING DATE: 04-APR-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L.
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 6362-52517
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619)238-0999
/ TELEFAX: (619)238-0062
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2161 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-455-543A-51

```

Query Match 7.2%; Score 190; DB 1; Length 2161;  
 Best Local Similarity 18.5%; Pred. No. 1.8e-09;  
 Matches 94; Conservative 83; Mismatches 155; Indels 176; Gaps 20;

```

QY 12 CRLGGWVPTGWRGELSLMGDPVWSCRFCSDQDDGDRRLTYFQNLPESTLSL 71
DB 333 CR--SGWVGPNCGI-----TNDNFAPFAMLTIV 357
QY 72 LVLLTANPDVMIPTAYSKNRAYA-----IFFTVTVIGSLFLMNLTLTIYSQFGYLM 126
DB 358 FOCITMEGTDLV---YWNDAIGWEPWYFVSLIIGSFVLNLVGLSGEFSKERE 414
QY 127 KSLQTSLFRRLGTAAFEVLSSWVG-----EGG-----APP----- 158
DB 415 KAKARGDFQKLRKQOLEEDLKGIDWITQAEIDPENEEGEGEGRKNTSMPTSESV 474
QY 159 -----QATRRGPSTSLRCPAPSSSATTTLTWTGSSPWOTWCF-----AC 201
DB 475 NTENVSGEGENRCCGSL--COAISKSK-----LSRRWRMRNRRRCRAAVKSV 523
QY 202 SMCWMOMCL--LSVMTSS-----WGF-----STASSLCTTQMSC-----CGRSLP--- 240
DB 524 TTYMLVIVLFTLITISSEHYNQDPWLQIODIANKVLALFTCEMLYKMSLGLQAYF 583

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0Y 241 -----NACBCTCTPATCTGSGSPSCMRPEMVGLSLMDMRMLNMLIVERPR 29
DB 564 VSLFNRFCFPVCCGCTITLIVLELMSPLG-----ISVRCVALLR 625
0Y 291 IIPSKMAVVAVSTVLGVONMRAFGGILVVVY--YFALLIGINLFRGYVALPGNSL 347
DB 626 IFKVRHMTSLSNLVASILNMSKIASLILLFLFIIFSLGMLQHLGRF----- 676
0Y 348 APANASCCSGFEOLEYANNPDEFAALVYIMLMVYNNMQ-VFLDAYRYSQPSK-- 404
DB 677 -----NFDEQTKRSTFDFNPQALLVFEQILTGEDMNAVMYDGIAYGPPSSGM 726
0Y 405 ---YFVLMMLVSSYIVNLFALILEN 429
DB 727 IVCITFIILFCIGNTIILNVFLALAVDN 754

RESULT 5
US-08-223-305C-49
: Sequence 49, Application US/08223305C
: Patent No. 5851824
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/223,305C
: FILING DATE: April 4, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/866,354
: FILING DATE: April 10, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/116,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 52516 (P519739)
: TELECOMMUNICATION INFORMATION:

```

```

/ TELEPHONE: (619)238-0999
/ TELEFAX: (619)238-0062
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2161 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
US-08-223-305C-49

Query Match 7.2%; Score 190; DB 2; Length 2161;
Best Local Similarity 18.5%; Pred.No.1.8e-09;
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGWMPPTWVWVAGLESLMGDPVYPMSCFCSQDDDGODRRLYYFOALPSPSL 71
DB 333 CR--SGWGPNGI-----TTFDFAFAMLTIV 357
QY 72 IYLLFTANPDWIPAYSKNRAYA-----IFFYFVIGSLFMLNLTAIISOPRGYLM 126
DB 356 FCGITMEGTIDLV---YMNNDAMGELPWPYIVSVLIGSFYVNLVLGVLSEGFSKERE 414
QY 127 KSLQTSLEFRRRLGTRAAFEVLSSWVG-----EGG-----AFP----- 158
DB 415 KAKAGDFOKLTREKQQLLEEDLKGVDWITQAEIDIDPENEEGEGEKRTYSMPTSETESV 474
QY 159 -----QATRGPTSLRFCRAPSSSASTTTLLTWGSSPWQTCPF-----AC 201
DB 475 NTEVNSGEEENGGCCGSL--COAISKSK-----LSRRRRNRNRNRRCRAVKS 523
QY 202 SMCWQMOMCCL-LSVWTTSS-----WGF--STASSLCTTCWSC-----CSRSLP--- 240
DB 524 FRYWLVIVLVFNLTLTISEHYNQPDWLTQIDIANKVLALFTCEMLVKYMSLGDAQYF 583
QY 241 -----WACBETCPPATCUTGSSPSLSCWRPEWAGLSLMDTKLNLIVFRFLR 290
DB 584 VSLNRPDCEYVGGGITEFIIIVELIEMSPLG-----ISVRCVRLLR 625
QY 291 IIPSKMAVNAVSVTLGVQNMRAAGGLIVVY---YFAIIGINLFRGVIALPGNSSL 347
DB 626 IEFKVRHMTSLSLNVLASILNLSKMSIASILLLLFLFTIIIFSLGMLPFGKPF----- 676
QY 348 APANGSAPCGSEQLLEYMANNFDDFAALVTLMLNLVNNMO--VFLDAYRRYSGEWSK-- 404
DB 677 -----NDEDTQTRKSTEDNFPQALLVFOILTGEDMNNAVYDGIAMVGGPSSSGM 726
QY 405 ---IYEVLMWLVSSVIVWNLFLALLLN 429
DB 727 IVCITFIIFLCGNITLLNVLALAVDN 754

RESULT 6
US-08-223-305C-51
Sequence 51, Application US/08223305C
Patent No.5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA

```







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; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1873 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-435-675B-4

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Query Match      7.1%; Score 186; DB 1; Length 1873;
Best Local Similarity 18.1%; Pred. No. 3.6e-09;
Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;

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QY 58 LTYFQNLPESTLVLTLTANNDVMPAYSKNRAVA-----IFIVFTVGLSLFLML 112
DB 272 ITHFDNFGFEMLVYOCITHEGTDVL---YWNDAIGEMWPVYVTLTLLGSFELML 328
QY 113 LTIITISQFGYLMKSLQSLFRRRLGTRAPEVLSSNVG----- 152
DB 329 VLDVLSGEFTKEREKAKSGTFQKLEKQOLEEDLGRYMSWITIGFVMDVEDLRECKLSL 388
QY 153 -EGGAPQATR--RGPSTSLRFRAPSSSATTTLTWTGTSFQWTW---CPACS---- 202
DB 389 EEEGSTESLEYELGLINKITIOFIR-----HWRQWNVFPMKCHDLVK 430
QY 203 ---WCMQMC-----CLTSVMT-----SSWGPSTAS 225
DB 431 SRVFLVILVALNTLSIASEHNQPLVTLHODIANVLLSLTIEMLMGLGLRQ 490
QY 226 SLCT-----TCMSCGRSLP--WACGCTPTPATCITLGSPLSCWRPEVGLSLMDMTFM 279
DB 491 YEMSIENRDCFVYCGILLLVSGAMTP---LGISVLRC----- 529
QY 280 LMLLYFRFLRIIPSKPAVAVSVYGLVOMRAFGILVYV---YVFAIIGINLRG 336
DB 530 -----IRLLRLFKITKYTSLSNLVASILNSIRIASLILLFLFIIFALLGMLFGG 583
QY 337 VIVALPGNSSLAPANGSAPCGSFQOLEYVANNFDDFAALVTLMLMVVNNM--QVFLDAY 395
DB 584 RV-----DFEDTEVRSNFDNFPQALLSVFQVLIGEDMNSMNYGI 624
QY 396 RRYSGPWSK-----TYFVIMLVSSVIVNLFALILENFLH-----KMDPSHL 440
DB 625 MAYGGPSIVGVLCIYFIIFLCGVYILINVLAIADNLEAESLTSQAKAKEERRRR 684
QY 441 OPLAGTPEATYOMTEVLELFRDILEEPGEDELETERLSQHP 479
DB 685 KMSRGLPKT-----DEEKSVAKKLEQKP 709

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RESULT 10
US-07-745-206A-13
; Sequence 13, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann

```

```

; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-13

```

```

Query Match      7.0%; Score 185.5; DB 1; Length 1754;
Best Local Similarity 24.6%; Pred. No. 3.7e-09;
Matches 83; Conservative 54; Mismatches 141; Indels 59; Gaps 13;

```

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QY 149 SMVGGGAFPOAT-----RR-----GPSISLAFCR-APSSSATTTLTWTG 188
DB 1082 ALDGKPRSEFVYVWTWKAKQGRRRMRKMGADGLSHTPACSVAPPTCSASATSPG 1141
QY 189 TSSPQWTW--CPFACSWCMQMCCLSVMT---SSWGFSTASL---CTTSCGCRSLPWA 242
DB 1142 TSRNFSWSSPAASPMLRTOCAQTRGTTLNTYITSLVSLPRMNSTWDCCGTLEP-- 1199
QY 243 CEGTCPTPATCITLGSPLSCWRPEVGLSL-----WDMTRMLMLYFRFLRIIPSKP 297
DB 1200 ISGTCGTFWTSIMSVAP--WWR-----LTSRKGKDINTIKSLVLRVLRPLKIRLPK 1252
QY 298 MAVAVSVYGLVOMRAFGILVYVVPALICINLFRGIYVALPGNSSLAPANGSAPCG 357
DB 1253 LKAIFDVCVNSLKVALLIYVLMFETFAVIAQLFKGKFFYCTDSKLEBDCRGQYL 1312
QY 358 SFQOLEYWAN-----NEDDFAALVTLMLMVVNNQVFL---DAYRRYSGPWS- 403
DB 1313 DYKEEVEAQRQMKYDHFYDNLVALLLFLFYSGEGPMVLKKSVDATYEOGSPSG 1372
QY 404 -----KIYFVIMLVSSVIVNLFALILENFLHKWD 435
DB 1373 YRMELSTFYVYVVFPPFFVNIFVALIITTFQEOGD 1409

```

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RESULT 11
US-08-311-363-13
; Sequence 13, Application US/08311363
; Patent No. 5876938
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert

```

TITLE OF INVENTION: Human Calcium Channel Compositions and  
METHODS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,363  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-51506  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0099  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1754 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-311-363-13

Query Match 7.0%; Score 185.5; DB 2; Length 1754;  
Best Local Similarity 24.6%; Pred. No. 3.7e-09;  
Matches 83; Conservative 54; Mismatches 141; Indels 59; Gaps 13;

QY 149 SMWGGAFAFOAT-----RR-----GPSISLRRCR-APSSSATTTLTWTG 188  
DB 1082 ALLEGKPRSPFVVTWTKAKGRRRMRMTGAAPGLSSHTAPCSVAAPTCASASATTSPG 1141  
QY 189 TSPWQW-CPPACSMCMQMCCLLSVMT--SSWGCFSTASSL--CTTCWCCSRLPWA 242  
DB 1142 TSKRSEFMSHSPASPMILRQCOQTRGTLNLTWTFSLVSLRLMRSTWDCFTLEP-- 1199  
QY 243 CEGTCPPATCLGSSPLSCWRPBNGLSL-----WDMTRMLNMLIVFFFLIITSMP 297  
DB 1200 ISGTCGFMTSLMSVAP--MWR-----LRSRSGKGDINTIKSLRVLRPLTKIRLPK 1252  
QY 298 MAVVASVVLGIYQNMRAFGLIVVVYVVFALIGINLFRGIVVALPGNSSIAPANGSAPCG 357  
DB 1253 LKAIVEDCVNSLKNVNLILVYLMFETFAVIAVLQFKGFFCTDESKLEDCGQYL 1312  
QY 358 SFEOLEYMAN-----NEDDEPAALVTLMLNLMVNNQVFL---DAYRRYSGPWS- 403  
DB 1313 DYKEEVEAQRQKMKYDFHNDVLMALLLFTFVSTGECPMVLKHSVDATYEQGPSFG 1372  
QY 404 -----KIYFVLMVLVSVIVNLFALILENFLHKMD 435  
DB 1373 YRMELISIFVYVYFVFFEFVNIIFVALIITFORQGD 1409

RESULT 12  
US-08-455-543A-45  
; Sequence 45, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0099  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1968 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-45

Query Match 6.8%; Score 178.5; DB 1; Length 1968;  
Best Local Similarity 18.4%; Pred. No. 2.1e-08;  
Matches 104; Conservative 80; Mismatches 175; Indels 205; Gaps 23;

QY 46 CSQDDGQDRERLTYFQNLPELSLTLVLLTTANNPDVIMIPYSKNRAVA-----IFFIV 100  
DB 332 CKRGWG-PKHGTINDNDAFAMLVFCITWEGWTDVL---YVNDAGRDMPWITYFTV 387  
QY 101 FTVIGSLFTMLTALITIQF-----RGYLMKSLQTSLE 134  
DB 388 LIIIGSFVNLVGLVSGEFSKREKARAGDFQRLKQOLEBDLGYLDWITQADBI 447

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QY 135 R-----RRIGTRAFAEVLSSWVGGAFAPOATR-----162
Db 448 XPENDEGMDKEERPNRGTGAG--MLDOKKGFAMFHSSTETHVSMPTSETESVNTENVA 505
QY 133 -----RGPTSLRFGCAPSSSATTTTLTWTGTSPPWQTCPPACSMC-----MMOM 208
Db 506 GGDIEGNCAGLAHRISKSK-----FSRYWRNRNRCRRKCRRAAVSNVFWMLVI 556
QY 209 -CCLLSVMT-----SSW-----GFSTASSICT-----229
Db 557 FLVPLNTLTIASSEHYNOBNMLEVODTANKALLLFTAEMLLKKYSLGLQAYFVSLNRF 616
QY 230 TCMSCCSRLPWACGCTPTPATCUTGSSPLSCWRPEVGLSLMDTMRMLNMLIVERFL 289
Db 617 DCFVVCGLLETL--LVEIKIMSPGLISVLR-----VRLLRIFKTRWNSL-----662
QY 290 RIIPSMKMAVAVASTVGLVONMRAFGIIVVY--YVFAIIGINLFRGIYALPQNSS 346
Db 663 -----SNLVASLNSVRSIASLILLLFLFLIFLIFSLGMQLFGKF-----702
QY 347 LAPANGSAPCGSPOLEYMANFDDFAALVTMLNMLVNNW--OVFLDAYRRYSGPWSK- 404
Db 703 -----NDEMOTRSTPTNFQSLITVFOILLGEDMNSVMYDGMAYGGPSPFG 751
QY 405 ----IYVLMWLVSSVIVMNLFLALILENF-----LHKMDPRSHLOPLAGT--PEA 449
Db 752 MLVCIYFIILFISGNVILLNVLAIADVNLADBSLTSALKKEEERKRLARTASPER 811
QY 450 TYQMTVELLFRDILEEPEDELE 473
Db 812 K-----QELVEKPAVGSKE 826

RESULT 13
US-08-223-305C-45
; Sequence 45, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1968 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-223-305C-45

Query Match 6.8%; Score 178.5; DB 2; Length 1968;
Best Local Similarity 18.4%; Pred. No.2,1e-08;
Matches 104; Conservative 80; Mismatches 175; Indels 205; Gaps 23;

QY 46 CSQDDGCDREKLYFONLPESLTLVLLTANNPDVIMPAYSKRNRYA-----IPEIV 100
Db 332 CKPWMDG--PKHGITNDFNFAFMLTVFOCITMEGWTDLV--YVNDAYGRDMPWYIVYT 387
QY 101 FTVIGSLFLMNLITFAIIVSOF-----RGYLMKSLQTSLE 134
Db 388 LIIISFVLNVLVGLVSGFSKEREKAKAGDFOKLEKQLEBDLGYIDMTQADBI 447
QY 135 R-----RRIGTRAFAEVLSSWVGGAFAPOATR-----162
Db 448 XPENDEGMDKEERPNRGTGAG--MLDOKKGFAMFHSSTETHVSMPTSETESVNTENVA 505
QY 133 -----RGPTSLRFGCAPSSSATTTTLTWTGTSPPWQTCPPACSMC-----MMOM 208
Db 506 GGDIEGNCAGLAHRISKSK-----FSRYWRNRNRCRRKCRRAAVSNVFWMLVI 556
QY 209 -CCLLSVMT-----SSW-----GFSTASSICT-----229
Db 557 FLVPLNTLTIASSEHYNOBNMLEVODTANKALLLFTAEMLLKKYSLGLQAYFVSLNRF 616
QY 230 TCMSCCSRLPWACGCTPTPATCUTGSSPLSCWRPEVGLSLMDTMRMLNMLIVERFL 289
Db 617 DCFVVCGLLETL--LVEIKIMSPGLISVLR-----VRLLRIFKTRWNSL-----662
QY 290 RIIPSMKMAVAVASTVGLVONMRAFGIIVVY--YVFAIIGINLFRGIYALPQNSS 346
Db 663 -----SNLVASLNSVRSIASLILLLFLFLIFLIFSLGMQLFGKF-----702
QY 347 LAPANGSAPCGSPOLEYMANFDDFAALVTMLNMLVNNW--OVFLDAYRRYSGPWSK- 404
Db 703 -----NDEMOTRSTPTNFQSLITVFOILLGEDMNSVMYDGMAYGGPSPFG 751
QY 405 ----IYVLMWLVSSVIVMNLFLALILENF-----LHKMDPRSHLOPLAGT--PEA 449
Db 752 MLVCIYFIILFISGNVILLNVLAIADVNLADBSLTSALKKEEERKRLARTASPER 811
QY 450 TYQMTVELLFRDILEEPEDELE 473
Db 812 K-----QELVEKPAVGSKE 826

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RESULT 14  
US-08-455-543A-48  
Sequence 48, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455, 543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2237 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-48  
Query Match 6.7%; Score 175.5; DB 1; Length 2237;  
Best Local Similarity 19.6%; Pred. NO. 5.1e-08;  
Matches 105; Conservative 89; Mismatches 184; Indels 157; Gaps 24;

QY 36 DPVVPWSC-----RRCSDODGODRE-----RLTYEQNLPESTLSLLVLTANNP 82  
DB 261 EPVGDPEPCKEAPARLC--EGDTECREYMPGPRFGITNDNLLFALTYGQITMEGWD 318  
QY 83 VMIPAYSKNRAYA-----IEFIVFYIGSLFNLMLTAITYSOF-----RGYLMK 127  
DB 319 IL---YNTDAAGNTWMWLIYFIPLIIGSFMLNLVIGYSGFAKERERVENRAFLK 375  
QY 128 SLOTSLEFRRLG--TRAFAVELSSMGEGBGAPFATRGPGTSPRCRAPSSSATTLFT 186  
DB 376 RROOQIERELNGYLEWTFEKAEEVYLAEDR--NAEKSPLDVUK--RAATKSRNDLIHA 431  
QY 187 WGTSSPMQWC---PF-----ACSNQWQMC- 209  
DB 432 EGEDRADLCVAGSPPARASLSKGTSESSYFRREKMPFRIRMYAQSFFYVVLVCV 491  
QY 210 -CLISVMTSSMGSTASSLCTTCWSCCSKSLPMACBGTCTPATC-LTGSPLSCWRPE- 266  
DB 492 VALNTLCVAMVHYNQPRRLTTLTYFA-----EVEFGLFTLEMSLKRYGLGPRSYRSSF 546  
QY 267 -----MVGILL--SLMDMTRM-----LNLIVFRFLRIPSKMPMAVAVSYGLVQYN 312  
DB 547 NCFDEGVIVGSVEFVVAALIKPSSSGISYLRALRLIRIKYKYSLSLNLVVSILNSK 606  
QY 313 RFGGILVVVY---YFPAIGINLFRGVIVALPONSLSLAPANGSAPCGSFQLEIYANNF 369  
DB 607 KSIISLFLFLFLFVFPALLGMQLFGQF-----NFQD-ETPTTNF 646  
QY 370 DDEPAALVTLMNLVANNVQVFLDAYRRY-----SGPMSKIYFVLMWLVSSYIVNLF 422  
DB 647 DTFPAAILTVFQILLTGEDMAVM--YHGISQGSVSGMSSFFLYLVLTFGNTTLNLF 704  
QY 423 LALILENFLHKWDRSHLOPLAGTEATYQMTVELFRDILIEEGEDELTERLSQ 477  
DB 705 LAIAYDN-----LANQDEL-----KDEEMEAANO 731  
RESULT 15  
US-08-223-305C-48  
Sequence 48, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991

Search completed: October 8, 2002, 10:06:49  
Job time : 31 secs

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0062  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2237 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-223-305C-48

Query Match  
Best Local Similarity 6.7%; Score 175.5; DB 2; Length 2237;  
Matches 105; Conservative 89; Mismatches 184; Indels 157; Gaps 24;

QY 36 DPVVPMS-----RFGSQDDGORE-----RLTYFQNLPESLTSLVLTATTANPD 82  
DB 261 EYVGDPECKEAPARLC-EGDTECREYWPGPFGITNFDNLFAILTVFCITMEGWD 318  
QY 83 VMIPAYSKNRAYA-----IEFIYFVIGSLFLMNLTLTAIYSQF-----RGYLMK 127  
DB 319 IL---YNTNDAGNTWMNMIYFIPLIIGSFENLVGLVGEFPAKERERVENRRAPFLKL 375  
QY 128 SIQTSIFRRRLG-TRAAFEVLSSWVEGGAFFQATRRGPSTSLRCPAPSSSSATTTLT 186  
DB 376 RROQOIERLNGYLEMIFKAEEVMLAEEDR--NAEKSPLDYLK--RAATKKSNDLIHA 431  
QY 187 WGTSSPMQWTWC---PF-----ACSWCMQMC- 209  
DB 432 EGEGERPADLCVGSFPFARASIKSGKTESSEYFRKREKMFRRFIRMWKAOSFYVVVLCV 491  
QY 210 -CLLSVMTSSWGFSTASSICTTCWSCCSRSIPWACEGTCPTATC-LTGSSPLSCWPE- 266  
DB 492 VALNTLCVAMVYNOPRRLTTLTYFA-----EFVFLGLFLEMSLKMTGLGPRSYFRSSF 546  
QY 267 -----WVGLL--SLUMDTKM-----LNMILVRFELRIIPSMKPMAYVASTVLGLVQNM 312  
DB 547 NCFDEGVTVGSVEYVMAIKPGSSFGISVLRALRLRIFFKVTYWSLSRLNLVYSLNSM 606  
QY 313 RAFGGLVVVY---YVFAIIGINLFRGYIVALPGNSSLAPANGSAPGSEQLLEYMANNF 369  
DB 607 KSIISLFLFLFLFIVFVALLGMQLFGGQF-----NFQD-ETPTTNE 646  
QY 370 DDEFAALVTLNLMVNNVNNVQVFLDAYRRY-----SGPMKIFYVLMVLVSSYIWNLF 422  
DB 647 DTFFPAITLVQIILGEDMNAVM--YHGESQGVSKGMFSSFYFIVLTJLGNNTLLNVF 704  
QY 423 LALILENPLHKWDRSHQPLAGTPEATYQNTVLLFRDILEPGEDELTERLSQ 477  
DB 705 LAIAVDN-----LANAOELT-----KDEEMEAAANO 731

•  
•  
•  
•

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 09:56:21 ; Search time 42 Seconds  
(without alignments)  
1109.603 Million cell updates/sec

Title: US-09-918-359-7  
Perfect score: 2634  
Sequence: 1 MSSACWEATGRCLGGGMV.....PGEDELTERLSQHPHMLCR 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1180	44.8	371	T46421	hypothetical prote
2	345	13.1	819	JC7240	two-pore calcium c
3	342	13.0	724	B65045	probable calcium c
4	197	7.5	2181	A38198	calcium channel al
5	194	7.4	2222	A37490	voltage-dependent
6	194	7.4	2272	C54972	voltage-dependent
7	190	7.2	1610	A46227	voltage-dependent
8	190	7.2	2161	JH0564	calcium channel al
9	189.5	7.2	2223	A47447	calcium channel pr
10	189.5	7.2	2262	T30890	calcium channel al
11	189	7.2	2270	A54972	voltage-dependent
12	187	7.1	2178	S29237	calcium channel pr
13	187	7.1	2259	S29236	calcium channel pr
14	186.5	7.1	2251	B54972	voltage-dependent
15	186	7.1	1873	A30063	dihydropyridine re
16	185	7.0	1646	JH0422	voltage-dependent
17	184	7.0	2220	A45290	calcium channel pr
18	180	6.8	2166	S11339	calcium channel al
19	179.5	6.8	2171	S05054	calcium channel al
20	178.5	6.8	2203	T42742	voltage-dependent
21	177	6.7	2139	A44647	voltage-dependent
22	176	6.7	1873	A5645	calcium channel, v
23	175.5	6.7	2237	T45115	N-type calcium cha
24	175.5	6.7	2339	A42566	omega-conotoxin-se
25	171	6.5	2254	T09053	low voltage-activa
26	168	6.4	2336	A45386	omega-conotoxin-se
27	167	6.3	1657	T15838	hypothetical prote
28	165.5	6.3	2143	JH0427	voltage-dependent
29	164.5	6.2	2273	JH4647	calcium channel BI

30	164.5	6.2	2424	2	146480	calcium channel BI
31	163.5	6.2	1687	2	S41742	calcium channel al
32	163	6.2	1852	2	A37860	calcium channel pr
33	161	6.1	1739	2	A48298	sodium channel hom
34	160.5	6.1	2108	2	S72458	sodium channel pro
35	160.5	6.1	2212	2	A41098	calcium channel pr
36	160	6.1	1559	2	T30535	calcium channel al
37	159.5	6.1	2019	2	A33996	sodium channel pro
38	159	6.0	274	2	E83837	hypothetical prote
39	159	6.0	1951	2	S00320	sodium channel pro
40	159	6.0	1983	2	A60054	sodium channel pro
41	158.5	6.0	1784	2	T43167	sodium channel pro
42	158.5	6.0	1810	2	T31092	probable voltage-g
43	158	6.0	1783	2	T37258	probable voltage-g
44	158	6.0	1917	2	C88728	protein C48A7.1 [i
45	156.5	5.9	2288	2	S41080	calcium channel al

## ALIGNMENTS

RESULT 1  
T46421  
hypothetical protein DKFZp434M0223.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46421  
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: 223034  
A:Accession: T46421  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-371 <AAA>  
A:Cross-references: EMBL:AL137479  
A:Experimental source: adult testis; clone DKFZp434M0223  
C:Genetics:  
A>Note: DKFZp434M0223.1

Query Match 44.8%; Score 1180; DB 2; Length 371;  
Best Local Similarity 99.6%; Pred. No. 1.4e-87;  
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 263 WRPEWGLSLDMTRMLNMLIVPFRLLRTPMKPAAVAVSVLGVOMRAFGILVYV 322  
DB 149 WRPEWGLSLDMTRMLNMLIVPFRLLRTPMKPAAVAVSVLGVOMRAFGILVYV 208  
OY 323 YVFAIIGINLFRGVYVALPGNSLAPANGSAPCGSFEQLEYWANNFDDFAALVTLMNL 382  
DB 209 YVFAIIGINLFRGVYVALPGNSLAPANGSAPCGSFEQLEYWANNFDDFAALVTLMNL 268  
OY 383 MYVNNWQVFLDLYRRYSRGSWSKIYFVLMVLSVIVNLFLLILENFIHKKDPSSHOP 442  
DB 269 MYVNNWQVFLDLYRRYSRGSWSKIYFVLMVLSVIVNLFLLILENFIHKKDPSSHOP 328  
OY 443 LAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHPHMLCR 485  
DB 329 LAGTPEATYQMTVELLFRDILEEPGEDELTERLSQHPHMLCR 371

RESULT 2  
JC7240  
two-pore calcium channel protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jun-2000  
C:Accession: JC7240  
R: Ishibashi, K.; Suzuki, M.; Imai, M.  
Biochem. Biophys. Res. Commun. 270, 370-376, 2000  
A:Title: Molecular cloning of a novel form (two-repeat) protein related to voltage-ga  
A:Reference number: JC7240  
A:Accession: JC7240  
A:Molecule type: mRNA  
A:Residues: 1-819 <ISH>

A:Cross-references: DDBJ:AB018253  
A:Experimental source: kidney  
C:Comment: This protein is a phosphorylated transmembrane glycoprotein having characteri  
C:Keywords: glycoprotein; kidney; transmembrane protein

Query Match 13.1%; Score 345; DB 2; Length 819;  
Best Local Similarity 25.7%; Pred. No. 7e-20;  
Matches 117; Conservative 71; Mismatches 164; Indels 104; Gaps 18;

QY 60 YFONPEBSLTLVLTANNPVMIPAYSKNRAVAIFVIVYIGSLFIMNLTAIYS 119  
DB 263 YFNTLSINVLNLTAAFPDPMPSYRNWCVFIVYILYILFIMNLTAIYV 322  
QY 120 QFNGYLMKSLQSLFRRLGTRAAFEVLSMVEGSAF-----POATRRGPST 167  
DB 323 TFDIEKHKFKSLLLKRLTAIOAHYHLVYQRRPAGISTYQFEGIMAFYPRASAR 379  
QY 168 SLRFPRASSSSATTTLT-----WGTSPPQW-----CPFACSMCMQMC 210  
DB 380 --RFLTFKALNQSNTPLLSLKDFYDIYEAALQMKAKKNQHWDELPRATFLFKG 434  
QY 211 LLSVMTSMGFSASSICT-----CW-----SCCRSLPMACEGCPPTACLT 255  
DB 435 -INILVNSKAFQYFMTLVAVANGVWILVETEMKGGFISKHVPWS-----LVFLTI 486  
QY 256 -----GSSPL-----SCWRP-----EMVGLSLMDMTMLM-----LIVFR 287  
DB 487 YGVELEPMKAVAGLDPVEELSSGMNLPDESLLAFALFLLAL-----TLNMPFYIVLR 541  
QY 288 --FLRIIPSKPMAYVASTYVLGVONKRAFGILVYVYFAITIGLFRGVI---VALP 342  
DB 542 LQLRFEKTKRRYRNVLDTFELLPRMASLGLTLTFEYFSAIVGMFFSGRLSPNCSTP 601  
QY 343 GNSSLAPANGS-APCGSEQL-----EYMANPDEFAALVTLNLMVYNNQVFLDAYR 397  
DB 602 ARRGLLPDSITRLGKTKFKGKGYIYLLNPNILNSFTLDELTVNNVYTIMESVTS 661  
QY 398 YSGPMSKIFVLMVLYSVIWNLFALILENPLK 433  
DB 662 QTSWISRLYPMFYITMVV-MTIYAFILLEAVFR 696

## RESULT 3

B85045  
probable calcium channel [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: B85045  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488  
A:Accession: B85045  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-724 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7270679; PIDN:CA877841.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4G03560  
A:Map position: 4

Query Match 13.0%; Score 342; DB 2; Length 724;  
Best Local Similarity 24.1%; Pred. No. 1.1e-19;  
Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;

QY 55 REBLYFQNLPEBSLTLVLTANNPVMIPAYSKNRAVAIFVIVYIGSLFIMNLTL 114  
DB 233 QOGLTFVTSYGATLYOMFIETTSNNDPMIPAYKSSRMSSVFVLYLVIGVFTNLIL 292  
QY 115 AIIYSQFRGLYMSLQ-TSLFRRLGTRA-----AEVYSS----- 149  
DB 293 AAVYDSFKQLAKOVSGMDQKRRMLEKAGLIDISKNGEIDKNOCIKLEQLTNYRTLP 352

QY 150 --MWEGGA-----PPQATRRGPST 167  
DB 353 KISKEEGLFLDELDTRDKINKDEFADLCQALALRFQKEVPSLEHFPQIYHSLSQ 412  
QY 168 SLR-FCRAPSSSA-----TTTLTWGTS--PMQWCPFACSMCM-MQMC 209  
DB 413 QLRASFVSPNFGVAISPLIINFLAVVETTLDEESSAQPMQV-AEFVGMIVYLEMA 471  
QY 210 CLLSVMT-----SSW--GFSTASSICTCWSCCRSLPMACEGCPPTATCLTGSSPLSCW 263  
DB 472 --IKIYYGFENWREGANFDLYT-----VVI--VIGTATPIT----- 508  
QY 264 RPEVGLSLMDMTMLMILVFRFLRIIPSKPMAYASTVLGVONKRAFGILVYV 323  
DB 509 -PENTFFSGEMIRYLLARMLRILFLMNVQRYRAFIITFLIPLSLMPTIGTICVL 567  
QY 324 YFPAIGINLFRGYVALPONSLSLAPANGSAPCGSEF---QLEYMANPDEFAALVTL 379  
DB 568 CIYCISIGVQVFGILVNA--GNKKL-----FETELAEEDYLLFNFDYPNMGVTL 614  
QY 380 WNLVYNNQVFLDAYRYSGPSKI-YFVLMVLYSVIWNLFALILENPLHKMD 435  
DB 615 FNLLVGMNQMVMESTKDLGTWMTSTYFVYITILLNLVAVFLAEAFTELD 671

## RESULT 4

A38198  
calcium channel alpha-1 chain, pancreatic - human  
N:Alternate names: Delta cell-type calcium channel alpha-1 chain; neuroendocrine-type  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
C:Accession: A38198  
R:Selino, S.; Chen, L.; Selino, M.; Blondel, O.; Takeda, J.; Johnson, J.H.; Bell, G.I.  
Proc. Natl. Acad. Sci. U.S.A. 89, 584-588, 1992  
A:Title: Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expres  
A:Reference number: A38198; MUID:92115705  
A:Accession: A38198  
A:Molecule type: mRNA  
A:Residues: 1-2181 <SEI>  
A:Cross-references: GB:M83666; NID:g179751; PIDN:AAA5629.1; PID:g179752  
A:Experimental source: pancreatic beta cells  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C:Keywords: membrane protein; voltage-gated ion channel

Query Match 7.5%; Score 197; DB 2; Length 2181;  
Best Local Similarity 18.2%; Pred. No. 1.7e-07;  
Matches 93; Conservative 81; Mismatches 175; Indels 162; Gaps 17;

QY 12 CRUGGMMVPTGMYRGLELSLMGDDPVYPMWSCRCSQDDGODRRLTYFQNLPESTLSL 71  
DB 333 CR--SGWVGPNGI-----TNDNFAMFLAVT 357  
QY 72 LVLLTTANNPDMIPAYSKNRAVA-----IFVIVYIGSLFIMNLTAIYQFRGYLM 126  
DB 358 FOCITMEGWDVL--YVWVDAIGWEMPMVYFVSLIIGSFNLNLVGLVSEF----- 409  
QY 127 KSLQTSLFRRLGTRAAFEVYSS-----MWEGGAFPOATRRGPSTSLRFC 172  
DB 410 -----SKERAKARAGDFQRLREKQLEEDLKGILDMITQAEIDIDPENEEGGEGRNT 464  
QY 173 RAPSSSATTTTLTWGTSPPMQWCPFACSMCMQMCCLLSVMTS--WGFSASSICT 229  
DB 465 SWPTSE--TESVMTENVVSGEGRGCGSLMCMWRRAKAKAPSGGRRWGQALISKSLS 522  
QY 230 TCSGCCSRSLPMACEGCPSPA-----TCLTGSSP----- 259  
DB 523 RRRRRNNRRRRRCRAAVKSVTFYVLYVLVFLNTLITLSEHYNODPWLQIODIANKVL 582  
QY 260 LSCWREP-----VGLSLMDM-----TRMLNMLIV-----FR 287  
DB 583 LALTECMYKMTSLGLQAVFVSLFNRFDCFYVCGGITETIIVELIEMSLGISVRCVR 642





R:Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.;  
Mol. Endocrinol. 6, 2143-2152, 1992  
A:Title: Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel fro  
A:Reference number: A46227; M0ID:93149124  
A:Accession: A46227  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1610 <YAN>

A:Experimental source: insulin-secreting cell line HIT-T15  
A:Note: sequence extracted from NCBI backbone (NCBI:P123692)  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 7.2%; Score 190; DB 2; Length 1610;  
Best Local Similarity 17.9%; Pred. No. 4.5e-07;  
Matches 91; Conservative 86; Mismatches 174; Indels 158; Gaps 18;

QY 6 WEATGR-CRLGG-----GMVPPGVRGLSLMGLGDPVYWSCRCQDDGDRRLT 59  
DB 318 FSGNGRCVAVNGTECRSGVWPNNGI-----T 344  
QY 60 YFONLPESLTLVLTANNPDVIMPAYSKNRAYA-----IFPVTYIGSLFIMNLT 114  
DB 345 NEDFAPAMLVFOCITMEGTDLV---YMNDAAGFELPWYFVSLVIGSFVNLVL 401  
QY 115 AIISQFQYLMKSLQTSLEFRRLGTRAFEVLSMWG-----EGAFPPQA 160  
DB 402 GVLSEGESEKREKAKAGDQKLENEQLEDLKGYLDWITQADIDPENEEGEGEGKR 461  
QY 161 TRRQPSLSLRCPAPSSSATITLTWGT-----SSPQWQCFP-----A 200  
DB 462 NTSMTSETESVNTENYSGEGTQSGSLQALSKSLSRMRMRNRFRRCRAVKS 521  
QY 201 CSMQWMOCL-LSVMTSS-----WGF-----STASSLCTTQWSC-----CSRSLP-- 240  
DB 522 VTFWLVIVLVFNTLTISSEHYNPQDMLQIODANKVLLAFTCEMLYKMTSLGQAY 561  
QY 241 -----WACEGTCPPATCLTGSSPLSCWRPEWGLSLMDTRLMLLYFRFL 289  
DB 562 FVSLFNRFDFVCGGITETILVELLMSPLG-----VSFRCVRL 623  
QY 290 RIISMKPMVAVASTVIGLVONMRAFGILVYV---YFAIIGINLFRGVIALPQNS 346  
DB 624 RIFVTRHMTSLSLNVLASLNSKMSIASLLFLFLIIFSLGMLFGKRF----- 675  
QY 347 LAPANGSAPCGSFQOLEYMANNDFAALVTLMNLVNVNMQ-VFLDAARRSGPMSK- 404  
DB 676 -----NPDETQKRTSTFDFNFQALLTVFOILTGEDMNAVMYDGMAYGSPSSG 724  
QY 405 ---IYFVLMVLVSSVIMVNLFLALLEN 429  
DB 725 MIVCIYFIILFCIGNYILLNVLAIADN 753

## RESULT 8

JH0564  
calcium channel alpha-1D chain - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 24-Nov-1999  
C:Accession: JH0564  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellistelet, G.; Ellis, S.B.;  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of a  
A:Reference number: JH0564; M0ID:92110010  
A:Accession: JH0564  
A:Molecule type: mRNA  
A:Residues: 1-2161 <WIL>  
A:Cross-references: GB:M76558  
A:Experimental source: neuroblastoma, cell line IMR32  
C:Comment: This protein is a subunit of the voltage-dependent calcium channel.  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C:Keywords: transmembrane protein  
F:127-145/Domain: transmembrane #status predicted <IS1>  
F:164-183/Domain: transmembrane #status predicted <IS2>

F:195-214/Domain: transmembrane #status predicted <IS3>  
F:236-254/Domain: transmembrane #status predicted <IS4>  
F:274-293/Domain: transmembrane #status predicted <IS5>  
F:382-406/Domain: transmembrane #status predicted <IS6>  
F:524-542/Domain: transmembrane #status predicted <IS7>  
F:558-577/Domain: transmembrane #status predicted <IS8>  
F:586-603/Domain: transmembrane #status predicted <IS9>  
F:615-633/Domain: transmembrane #status predicted <IS10>  
F:653-672/Domain: transmembrane #status predicted <IS11>  
F:728-752/Domain: transmembrane #status predicted <IS12>  
F:888-905/Domain: transmembrane #status predicted <IS13>  
F:922-941/Domain: transmembrane #status predicted <IS14>  
F:954-972/Domain: transmembrane #status predicted <IS15>  
F:980-998/Domain: transmembrane #status predicted <IS16>  
F:1018-1037/Domain: transmembrane #status predicted <IS17>  
F:1128-1152/Domain: transmembrane #status predicted <IS18>  
F:1206-1224/Domain: transmembrane #status predicted <IS19>  
F:1240-1259/Domain: transmembrane #status predicted <IS20>  
F:1268-1286/Domain: transmembrane #status predicted <IS21>  
F:1315-1333/Domain: transmembrane #status predicted <IS22>  
F:1353-1372/Domain: transmembrane #status predicted <IS23>  
F:1440-1464/Domain: transmembrane #status predicted <IS24>

Query Match 7.2%; Score 190; DB 2; Length 2161;  
Best Local Similarity 18.5%; Pred. No. 6.1e-07;  
Matches 94; Conservative 82; Mismatches 156; Indels 176; Gaps 20;

QY 12 CRLGGWVPTGVNVRGLSLMGLGDPVYWSCRCQDDGDRRLTYFQNLPELSL 71  
DB 333 CR--SGWCPNNGI-----INFDFAPAMLTIV 357  
QY 72 LVLLTANNPDVIMPAYSKNRAYA-----IFPVTYIGSLFIMNLTALYISQFQYLM 126  
DB 358 FQGITMEGTDLV---YMNDAAGFELPWYFVSLVIGSFVNLVLVIGSEFSEKRE 414  
QY 127 KSLQTSLEFRRLGTRAFEVLSMWG-----EG-----AFP----- 158  
DB 415 KAKARGDFKLEKQLEDLKGYLDWITQADIDPENEEGEGEGKNTSMPTSETESV 474  
QY 159 -----QATRRQPSLSLRCPAPSSSATITLTWGTSSPQWQCFP-----AC 201  
DB 475 NTEVNSGEGENKCCGSL--CQALSKSK-----LSRRRRRRRRRRRCRAVMSV 523  
QY 202 SMCWMOCL-LSVMTSS-----WGF-----STASSLCTTQWSC-----CSRSLP-- 240  
DB 524 TFWLVIVLVFNTLTISSEHYNPQDMLQIODANKVLLAFTCEMLYKMTSLGQAY 583  
QY 241 -----WACEGTCPPATCLTGSSPLSCWRPEWGLSLMDTRLMLLYFRFL 290  
DB 584 VSLFNRFDFVCGGITETILVELLMSPLG-----ISVRCVRLR 625  
QY 291 RIISMKPMVAVASTVIGLVONMRAFGILVYV---YFAIIGINLFRGVIALPQNS 347  
DB 626 IFKVTIRHMTSLSLNVLASLNSKMSIASLLFLFLIIFSLGMLFGKRF----- 676  
QY 348 APANGSAPCGSFQOLEYMANNDFAALVTLMNLVNVNMQ-VFLDAARRSGPMSK-- 404  
DB 677 -----NPDETQKRTSTFDFNFQALLTVFOILTGEDMNAVMYDGMAYGSPSSG 726  
QY 405 ---IYFVLMVLVSSVIMVNLFLALLEN 429  
DB 727 IYCIYFIILFCIGNYILLNVLAIADN 754

## RESULT 9

A47447  
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommat  
C:Species: Discopyge ommata  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999  
C:Accession: A47447  
R:Horne, W.A.; Ellinor, P.T.; Iman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993  
A:Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray D

A:Reference number: A47447; MUID:93248175

A:Accession: A47447

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2223 <ORF>

A:Note: sequence extracted from NCBI backbone (NCBI:130671)

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 7.2%; Score 189.5; DB 2; Length 2223;

Best Local Similarity 19.9%; Pred. No. 6.9e-07;

Matches 107; Conservative 87; Mismatches 197; Indels 147; Gaps 25;

```

QY 43 CRRCSQDQDQRRITTYQNPESITSLVLTANNPDVIMPAKRNRAVA-----IF 97
DB 291 CSYWGIPNDG-----ITQFDNIFALTFVQCITMEGWTTL--YNDLALGAMWMLV 342
QY 98 FIVFVIGSLFLMNLTLTIYSQF-----RGYLMKSLQTSIFRRRLGTRA---A 143
DB 343 FIPLIIGSFYVNLVGLVSGEFAKERERVENRRSFLKRRQOIERELNGYRAMIDKA 402
QY 144 FEVL-----SSMYEGGAFPOATRNG--PSTSLRFRAPSSSAATTLTWTGSSP----- 192
DB 403 EYVMLEENKNAKESKAL--HYLRATIKKGRMIQTSSSDQYIEISSV--SPLARAS 459
QY 193 -----W-----QTWCPFACSW---CMQ 207
DB 460 IKSTKLEGGSSYFRKKEMLRISIRHWKSHAFYIVLGLVALTVCVAVVHYDQPLMLLS 519
QY 208 MCCLISVMTSSWGEFSTASSLCTTCWSCSRSLPACCEGTCTPATCLTGSSPLSCWR--PE 266
DB 520 NEFYAETFTGLFS--SEMFLLKMYGGPR-----LYHSSFECEFCQGV 561
QY 267 MVGLL--SLMDTRM-----LNLIVFRFLIIPSKPMVAVSTVLGLVONMRAFGIL 319
DB 562 IIGSIFDVVYITIPETSGISVLRALRLRIFKITYKMASLRNLVYLSMSKSIISL 621
QY 320 VVYV--YVFAIIGINLFRGYVALPGNSSLPANGSAPGSGFQLEVMANNDDPAAL 376
DB 622 FILFLFVFFALCMQLEFG-----QPNPEEGTTP-----TNDTTPPAI 661
QY 377 VTLMNLMVNNM--QVFLDAVRRY---SGPWSKIYFVLMVLSVIVNLFALLILENFL 431
DB 662 ITVFQILTGDEWMEVMYNGIKSGGVGMSWYFIVLTLFNGYTLNLFALIAVDNLA 721
QY 432 HKMDPRSHLOPLAGTPATYQMTVELFRDI--LEEGDELTERRLSQPH--LMLCR 485
DB 722 NAQELTKEEQE---EEBAIQKHALQAKAEVSPASGPEPSTERFRHRHMSWEAR 776

```

# RESULT 10

T30890

calcium channel alpha1-chain - sea squirt (Halocynthia roretzi)

N:Alternate names: ascidian calcium channel alpha1-subunit

C:Species: Halocynthia roretzi

C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000

R:Okamura, Y.; Okagaki, R.

submitted to the EMBL data library, May 1998

A:Description: TUCAL, ascidian calcium channel alpha1-subunit.

A:Reference number: Z20924

A:Accession: T30890

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2262 <OKA>

A:Cross-references: EMBL:AB013604; PIDN:BA434927.1

A:Experimental source: young tadpole larvae

A:Gene: TUCAL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: calcium binding; calcium channel

Query Match 7.2%; Score 189.5; DB 2; Length 2262;

Best Local Similarity 20.2%; Pred. No. 7e-07;

Matches 99; Conservative 76; Mismatches 159; Indels 157; Gaps 20;

```

QY 33 WGGDVPVWMSRFGS-----QDDGQDRERLTYQNPESITSLVLTANNPDVIMPA 87
DB 371 WG-----RCSGGMICESDWAGSPKGIINDFEYFAVITVQCITMEGWTDLV--- 418
QY 88 YSKNRAYA-----IFFIVFVIGSLFLMNLTLTIYSQFGRGYLMKSLQTSIFRRRLGTRA 142
DB 419 YNMDAVGNLMPWLYFSLIIGSFYVNLVGLVSGEFAKERERVENRRSFLKRRQOIERELNGYRAMIDKA 468
QY 143 AFEVL-----SSMYEGGAFPOATRNGP-----STSLRFRAPSSSAATTL 184
DB 469 EFQRLRKKQOTDEDMKGYMDITQAEIDLDPNEDREDRRSASNEQINDADSEVSGIQID 528
QY 185 TTWGT-----SSPQOTW-----CPF--ACSMQWOM--CCLISVMTSSW 219
DB 529 ETWQMQRALFKVCYRRRRRRNRKTRRCRKYVSKSPYVWLYVFCNTLSLATEHY 588
QY 220 GFSTASSLCTTCWSCSRSLPACCEGTCTPATCLTGSSPLSCWRPEM----- 267
DB 589 -----RQPPWL-----TLQDLANKILLITFTEMLYKMSLGMQY 625
QY 268 -VGLSLMD-----MTRM-----LNLIVFRFLIIPSKPMVAVSTVLG 307
DB 626 FVSLFNRFDFVCGGIVELVLTSSKIMEPLGISVLRVRLRLFRKMTSSMNSLMLVAS 685
QY 308 LVONMRAFGIIVVYV--YVFAIIGINLFRGYVALPGNSSLPANGSAPGSGFQLEBY 364
DB 686 LMSIRSISILVILFLFIIFALLCMQMEGGRF-----SEIQDEK 727
QY 365 WANNDDPAALIVTLMNLMVNNMOWF-----LDAYRRIS--GPWSKIYFVLMVLSVITW 418
DB 728 IRSNFTQIALTLVQILTGEDWVYVNGLEAVGASTIGLTSYFIVLFGNVL 787
QY 419 VNLFLALLEN 429
DB 788 LNVFLAIAVDN 798

```

# RESULT 11

A54972

voltage-dependent calcium channel alpha 1E-3 - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 24-Sep-1999

C:Accession: A54972

R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;

J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium chan

A:Reference number: A54972; MUID:94350992

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2270 <MTL>

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 7.2%; Score 189; DB 2; Length 2270;

Best Local Similarity 19.4%; Pred. No. 7.7e-07;

Matches 106; Conservative 91; Mismatches 218; Indels 132; Gaps 20;

```

QY 32 LMGGDPPVPMSCRRCSQDDQDQD---RERLTYQNPESITSLVLTANNPDVIMPA 87
DB 259 LEGFDPPHPCGVQCPAGYECKDWIGPNDDITQFDNIFAVLTFVQCITMEGWTYL--- 315
QY 88 YSKNRAYA-----IFFIVFVIGSLFLMNLTLTIYSQF-----RGYLMKSLQTS 132
DB 316 YNTNDALGATWMLTYFIPLIIGSFYVNLVGLVSGEFAKERERVENRRSFLKRRQOIERELNGYRAMIDKA 375
QY 133 LFRRRLCTRAAFVYSSWGEAGAFPOATRNGPSTSLRFRAPSSSAATTLTWTGSSP 192
DB 376 IERELNGYRAMIDKAEEVM-----LAEENKNACTSALEVLRATIRKSRTEATRTSSDPE 430
QY 193 W-----QTWCPFACSW-----WCMQMCCLISV--MTSS---WGFSTASSLCT 229

```

```

Db 431 HCVDISVGTPLARASIKSAKVDGVSFRHKKERLLRISIRHMKVSGFYIVLSTVALNT 490
QY 230 TCWCCSRSLP-WACE-----GTCPTPACLTGSSPLSCMR-P 265
Db 491 ACVAIVHNPQWTLHLIYAEPFLGLFLEMSLKMVGMPR---LYHSSFNCDG 546
QY 266 EMVGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVSTVLGVQNNRARGI 318
Db 547 VTGVSIFEVVAIRPGISFISVLRALRLIRIKTKYMASSLNLVLSMSKSIISL 606
QY 319 LVVYV---YVEAIGINLFRGVIALPGNSSLAPANGSAPCGSEQLEYANNEDDDPAA 375
Db 607 LFLFLFIVFALLGMQLFGFRFNFNDGTPSA-----NFDTPPAA 646
QY 376 LVTLNMLAVNNW-OVFLDAYRRY---SGPMSKIYFVLMVLSVNLFLALLENF 430
Db 647 IMTVFQILTGEDWNEVMYNGIRSGGVSSGMSAIFYFVTLFLFGVTLNVLALAVDNL 706
QY 431 L-----HKMDPRSHLOPLAGTPEATYQMTVELFRDLLEPGEDEL 471
Db 707 ANAQELTKDEEFAFNQKHALQKAKVSPMSAPNMPISIERRRRHMSWEPSSHL 766
QY 472 TERLSOH 478
Db 767 RERRRRH 773

```

## RESULT 12

S29237  
 calcium channel protein BII-2, brain - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
 C:Accession: S29237  
 R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.  
 FEBS Lett. 308, 7-13, 1992  
 A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit  
 A:Reference number: S29236; MUID:92354772  
 A:Accession: S29237  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-2178 <NII>  
 A:Cross-references: EMBL:X67856; NID:q1474; PIDN:CAA4804.1; PID:q1475  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
 C:Keywords: transmembrane protein

Query Match 7.1%; Score 187; DB 2; Length 2178;

Best local similarity 18.1%; Pred. No. 1.1e-06; Indels 162; Gaps 18;

Matches 102; Conservative 91; Mismatches 207;

```

QY 32 IMGDDPVVPMSCRFCSQDDGOD---RERLTYYFQNLPELSITSLVLTANNPDVMI 87
Db 259 LEGDPPHPCGVGCGPAGYECKMDIGPNDGITQFDNLFVAVLVCQITWEGTTLV--- 315
QY 88 YSKNRRAV---LFFIVFYIGSLFLMNLITAIYSQF-----RGYLMKSLQTS 132
Db 316 YNTNDALGATWNLTYFIPLIIGSFVNLVGLVLSGEFAKEREKREVENRRAFMKLRQOQ 375
QY 133 LFRRLIGTRAAFEVLSSWVGEGAFPOATRRGPSTSLFCRAPSSSATTTTLTWGTS 192
Db 376 IERELNGYRAWIDKAEVY---LAENKNSGSALEVLRRATIKRSRTAMTRDSSD- 429
QY 193 WQWCPFACSWCMQCCLSVMTSS----- 218
Db 430 -----EHCVDISVGTPLARASIKSAKVDGVSFRHKKERLLRISVRAVKS 475
QY 219 ---WGSTASSLCTTCWCCSRSLP-WACE-----GTCPTPA 251
Db 476 QVFWYIVLSTVALNTPCAVIVHNPQWTLHLIYAEPFLGLFLEMSLKMVGMPR-- 533
QY 252 TGLTSSPLSCMR-PEWVGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVS 303
Db 534 --LYHSSFNCDGVTGVSIFEVVAIRPGISFISVLRALRLIRIKTKYMASSLRN 591

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QY 304 TVLGVQNNRARGITLVVY---YVEAIGINLFRGVIALPGNSSLAPANGSAPCGSFE 360
Db 592 LVVLSMSKSIISLFLFLFIVFALLGMQLFGFRFNFNDGTPSA----- 638
QY 361 QLEYANNEDDDPAAALVTLNMLAVNNW-OVFLDAYRRY---SGPMSKIYFVLMVLS 415
Db 639 -----NFDTPPAAIMTVFQILTGEDWNEVMYNGIRSGGVSSGMSAIFYFVTLFLFGN 691
QY 416 VIVVNLFLALILENFL-----HKMDPRSHLOPLAGTPEATYQMTVE 456
Db 692 YTLNVLAVDNLNAOELTKDEEFAFNQKHALQKAEVSPMSAPNMPISIERRR 751
QY 457 LFRDLLEPGEDELTERLSOH 478
Db 752 RRRHMSWEPSSHLRERRRRH 773

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## RESULT 13

S29236  
 calcium channel protein BII-1, brain - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
 C:Accession: S29236  
 R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.  
 FEBS Lett. 308, 7-13, 1992  
 A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit  
 A:Reference number: S29236; MUID:92354772  
 A:Accession: S29236  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-2253 <NII>  
 A:Cross-references: EMBL:X67855; NID:q1472; PIDN:CAA4804.1; PID:q1473  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
 C:Keywords: transmembrane protein

Query Match 7.1%; Score 187; DB 2; Length 2259;

Best local similarity 18.1%; Pred. No. 1.1e-06; Indels 162; Gaps 18;

Matches 102; Conservative 91; Mismatches 207;

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QY 32 IMGDDPVVPMSCRFCSQDDGOD---RERLTYYFQNLPELSITSLVLTANNPDVMI 87
Db 259 LEGDPPHPCGVGCGPAGYECKMDIGPNDGITQFDNLFVAVLVCQITWEGTTLV--- 315
QY 88 YSKNRRAV---LFFIVFYIGSLFLMNLITAIYSQF-----RGYLMKSLQTS 132
Db 316 YNTNDALGATWNLTYFIPLIIGSFVNLVGLVLSGEFAKEREKREVENRRAFMKLRQOQ 375
QY 133 LFRRLIGTRAAFEVLSSWVGEGAFPOATRRGPSTSLFCRAPSSSATTTTLTWGTS 192
Db 376 IERELNGYRAWIDKAEVY---LAENKNSGSALEVLRRATIKRSRTAMTRDSSD- 429
QY 193 WQWCPFACSWCMQCCLSVMTSS----- 218
Db 430 -----EHCVDISVGTPLARASIKSAKVDGVSFRHKKERLLRISVRAVKS 475
QY 219 ---WGSTASSLCTTCWCCSRSLP-WACE-----GTCPTPA 251
Db 476 QVFWYIVLSTVALNTPCAVIVHNPQWTLHLIYAEPFLGLFLEMSLKMVGMPR-- 533
QY 252 TGLTSSPLSCMR-PEWVGLL---SLMDMTRM-----LNMIVFRFLRIIPSMKPAVAVS 303
Db 534 --LYHSSFNCDGVTGVSIFEVVAIRPGISFISVLRALRLIRIKTKYMASSLRN 591
QY 304 TVLGVQNNRARGITLVVY---YVEAIGINLFRGVIALPGNSSLAPANGSAPCGSFE 360
Db 592 LVVLSMSKSIISLFLFLFIVFALLGMQLFGFRFNFNDGTPSA----- 638
QY 361 QLEYANNEDDDPAAALVTLNMLAVNNW-OVFLDAYRRY---SGPMSKIYFVLMVLS 415
Db 639 -----NFDTPPAAIMTVFQILTGEDWNEVMYNGIRSGGVSSGMSAIFYFVTLFLFGN 691
QY 416 VIVVNLFLALILENFL-----HKMDPRSHLOPLAGTPEATYQMTVE 456

```

Db 692 YTLINFLAIVADNLANAQELTKDEGEFAFNOKHLOKAKVSPKAPVPSTIENDRR 751  
 QY 457 LIFPDILIEEGEDDELTERLSQH 478  
 Db 752 RHHMSWEPSSHLRERRRRH 773

## RESULT 14

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 24-Sep-1999

C:Accession: B54972

R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; M.J.

J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A:Reference number: A54972; MUID:94350992

A:Accession: B54972

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-2251 &lt;MIL&gt;

A:Cross-references: GB:129384; NID:9495867; PIDN:AA59204.1; PID:9495868

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

## Query Match

Best local similarity 7.1%; Score 186.5; DB 2; Length 2251;

Matches 98; Conservative 84; Mismatches 184; Indels 113; Gaps 19;

QY 32 LMGDPVPVPSRCFSCQDDGOD---REKLYFQNPESLTLTLTANNPDVWIPA 87  
 Db 259 LEEFDPHPGCGVCGAGYCKDWIGDITQFDNLFVAVLTVFCITMEGTTVL--- 315  
 QY 88 YSKNRVYA-----IEFIVTVIGSLFLMNLTAIYSQF-----RGYLMKSLQTS 132  
 Db 316 YNTNDALGATWMLYFIPILIISSFFVLNLVGLVSEFKEKEREVENRRAFMKLRQOQ 375  
 QY 133 LEFRRRLGTRAAFEVLSSMWEGGAFPOATRRGPSTSLRFRAPSSSATTLITWTGSSP 192  
 Db 376 IERELNGYRAMIDKAEVW-----LAEENKAGTSALEVARATIKRSKREAMTRDSSDE 430  
 QY 193 W-----QTMCPFACS-----WCWMOCCLSLV---WTS---WGFSTASSLCT 229  
 Db 431 HCVDISSVGTPLARASIKAKVDGVSFRHKEHLRISIHAWKSOVFYIVLSIALNT 490  
 QY 230 TCWSCCSSLP-WACE-----GTCPTPATCITGSSPLSCMR-P 265  
 Db 491 ACVAIYHNHQPWLTHLLTYAEFLGLLEMSLMTGMPR---LYFHSFNCDFEG 546  
 QY 266 ENVGGL--SLMDKTRM-----LMLIVFRRLIIPSMKPAVAVASTVLGVQMMRAFGI 318  
 Db 547 VIVGSIFFEVVWAIFRPGTSEGISLRLALRLRIFKITKYWASLRLNVLVSSMSKSLISL 606  
 QY 319 LVVVY---YVPAIIGINLFRGYVALPGNSSIAPANGSAPCGSEQLFTWANNFDDPAA 375  
 Db 607 LEFLFLFIYVFFALGMLQFLGGRFNENDGTPSA-----NFDFFPAA 646  
 QY 376 LVTLMNLAVVNMW-OVFLDAYRY---SGPMNKIYFVLMVLVSSVIVWNLFLALLEN 429  
 Db 647 IMTVFQILIGEDMNEVWYNGIRSGGVSSGMSAIFYIVLTFLGNTLLANVFLAIVDN 705

## RESULT 15

A30063

dihydropyridine receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Nov-1999

C:Accession: A30063

R:Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, V.; Takahashi, H.; Kangawa, K.; Kojima

Nature 328, 313-318, 1987

A:Title: Primary structure of the receptor for calcium channel blockers from skeletal mu

A:Reference number: A30063; MUID:87258269

A:Accession: A30063

A:Molecule type: mRNA  
 A:Residues: 1-1873 <TAN>  
 A:Cross-references: GB:X05921; NID:q1547; PIDN:CAA29355.1; PID:q1548  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
 C:Keywords: phosphoprotein; transmembrane protein

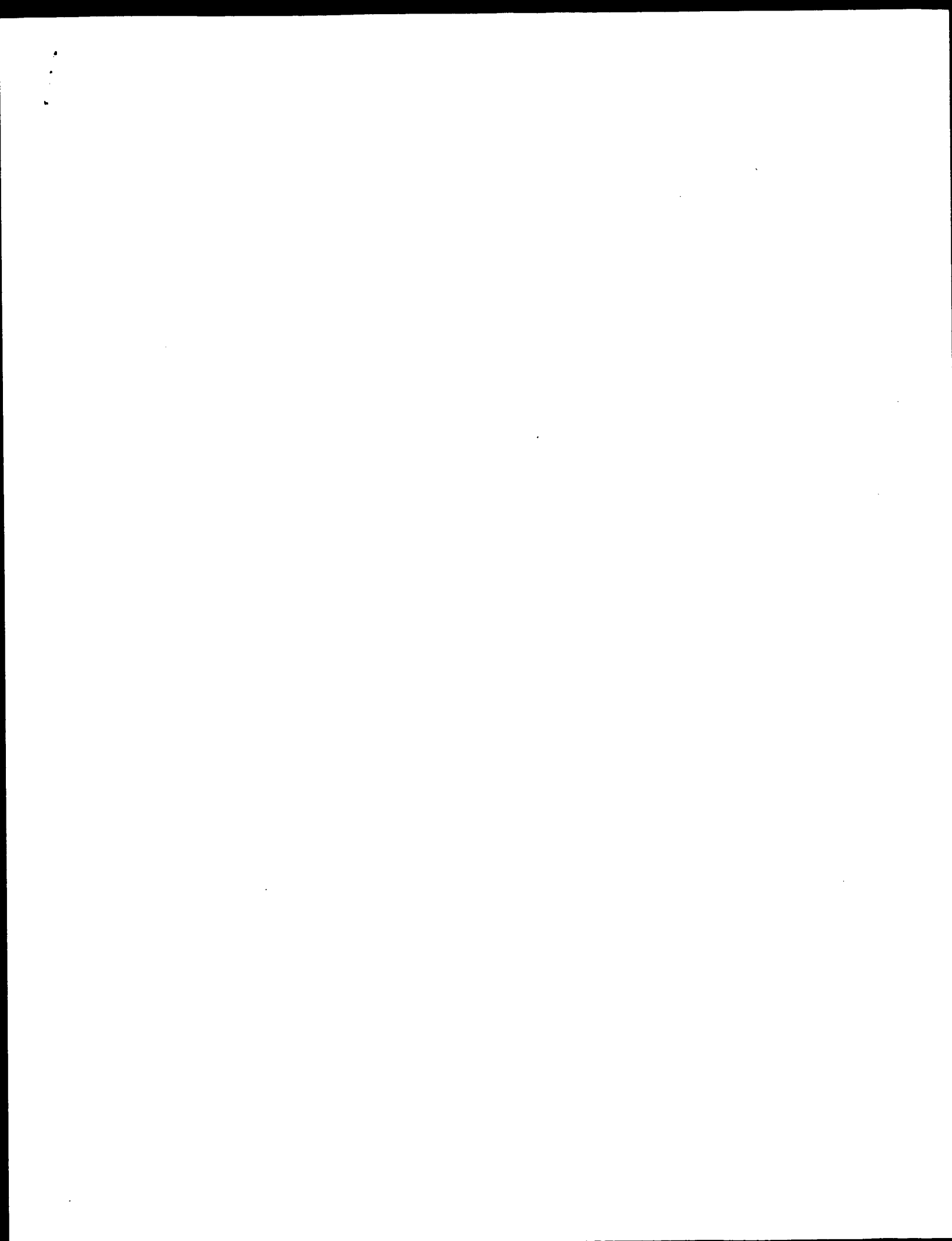
## Query Match

Best local similarity 7.1%; Score 186; DB 2; Length 1873;

Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;

QY 58 LTYFQNPESLTLTLTANNPDVWIPAYSKNRVYA-----IEFIVTVIGSLFLMNL 112  
 Db 272 ITHDNGFSLMLIYQCTITMEGTTDVL---YVNDALGNEMPMWIFVYLIIIGSFFIINL 328  
 QY 113 LTAIYSGFRGYLMKSLQTSLEFRRRLGTRAAFEVLSSWVG----- 152  
 Db 329 VLGVLSEFTYERKRAKSRGTFQKLRQKQLEEDLRGMSITQGEVWDVDELRGKSL 388  
 QY 153 -EGGAFPOATR--RGPSTSLRFRAPSSSATTLITWTGTSPPQW---CPFACS--- 202  
 Db 389 EEGSDTESLYEIDGLNKIIQFIR-----HRRQNRVFRMKCHDLVK 430  
 QY 203 ---WCWMOCC---CLLSYMT-----SSMGFSFNAS 225  
 Db 431 SRVFWVLIVALTSLIASHHNPLMTHODIANRVLSLFTIEMLMKMTGLGRLQ 490  
 QY 226 SLCT---TCWSCCSSLP-WACEGTCPTPATCITGSSPLSCMRPEWGLSLMDWTRM 279  
 Db 491 YFMSIFNRFQCFVYVCSGILLELLIVESGAMP---LGISVLRG----- 529  
 QY 280 LNMIVFRRLIIPSMKPAVAVASTVLGVQMMRAFGILVVY---YVPAIIGINLFRG 336  
 Db 530 -----IRLRLEKITYWTSLSNLWASLNSIRSLIASLILLFLFIIFALGMLQFLG 583  
 QY 337 VIVALPGNSSIAPANGSAPCGSEQLFTWANNFDDPAAALVTLMNLAVVNMW-OVFLDAY 395  
 Db 584 RY-----DFEDTEVRSNPNFQALISVQVLTGEDMNSVMYNGI 624  
 QY 396 RRYSGPMK---YFVLMVLVSSVIVWNLFLALILENPLH-----KWDPRSHL 440  
 Db 625 MAYGSPSPGVLCIYFIILFVCGNYLLANVFLAIVDNLAESLSAOKAKAEERKR 684  
 QY 441 QPLAGPEATYQMTVELLFRLDIEEGEDDELTERLSQH 479  
 Db 685 KMSRGLPDKT-----EEKSYWAKKLEQKP 709

Search completed: October 8, 2002, 10:06:01  
 Job time : 47 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 09:08:41 ; Search time 25 Seconds

(without alignments)  
751.159 Million cell updates/sec

Title: US-09-918-359-7

Perfect score: 2634  
Sequence: 1 MSSACWEATGRCLGGGMV.....PGEDELTERLSQHPHMLWLCR 485

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	7.6	2190	1	CCAD_CHICK
2	196	7.4	2169	1	CCAC_RAT
3	194	7.4	2222	1	CCAE_RAT
4	194	7.4	2272	1	CCAE_MOUSE
5	191	7.3	2312	1	CCAE_HUMAN
6	190	7.2	1610	1	CCAD_MESAU
7	189.5	7.2	2223	1	CCAE_DISOM
8	187.5	7.1	1966	1	CCAF_HUMAN
9	187	7.1	2161	1	CCAD_HUMAN
10	187	7.1	2259	1	CCAE_RABIT
11	186	7.1	1873	1	CCAS_RABIT
12	184	7.0	1873	1	CCAS_HUMAN
13	184	7.0	2221	1	CCAC_HUMAN
14	182	6.9	2339	1	CCAB_HUMAN
15	179.5	6.8	2171	1	CCAB_RABIT
16	178.5	6.8	2203	1	CCAD_RAT
17	177	6.7	2139	1	CCAC_MOUSE
18	175.5	6.7	2339	1	CCAB_HUMAN
19	175.5	6.7	2353	1	CCAB_HUMAN
20	171	6.5	2254	1	CCAG_HUMAN
21	171	6.5	2377	1	CCAG_HUMAN
22	170.5	6.5	1835	1	CCAI_RAT
23	169.5	6.4	2505	1	CCAA_HUMAN
24	168	6.4	2336	1	CCAB_RAT
25	167.5	6.4	2164	1	CCAA_MOUSE
26	165.5	6.3	2327	1	CCAB_MOUSE
27	164.5	6.2	2424	1	CCAB_RABIT
28	163.5	6.2	1687	1	CCAM_MOUSE
29	163	6.2	1852	1	CCAS_MOUSE
30	160.5	6.1	2212	1	CCAA_RAT
31	160	6.1	1951	1	CIN3_HUMAN
32	159.5	6.1	2019	1	CIN3_RAT
33	159	6.0	1951	1	CIN3_RAT

34	155.5	5.9	2516	1	CCAD_DROME	Q24270 drosophila
35	154.5	5.9	2016	1	CIN5_HUMAN	Q14524 homo sapien
36	148.5	5.6	1820	1	CINA_ELEEL	P02719 electrophor
37	148	5.6	2326	1	CCAB_DISOM	P56698 discopyge o
38	146	5.5	2131	1	CINA_DROME	P35300 drosophila
39	145.5	5.5	1848	1	CCAA_DROME	P91645 drosophila
40	145	5.5	2009	1	CIN1_HUMAN	P35498 homo sapien
41	145	5.5	2039	1	CCH1_YEAST	P50077 saccharomyc
42	144.5	5.5	2009	1	CIN1_RAT	P04774 rattus norv
43	142.5	5.4	2005	1	CIN2_RAT	P04775 rattus norv
44	142	5.4	1836	1	CIN4_HUMAN	P35499 homo sapien
45	139	5.3	1146	1	CCAS_RAT	Q02485 rattus norv

## ALIGNMENTS

RESULT 1  
ID CCAD\_CHICK STANDARD; PRT; 2190 AA.  
AC 073700: 073701: 073702: 073703: 073704:  
DT 15-JUL-1999 (Rel. 38, created)  
DT 15-JUL-1999 (Rel. 38, last sequence update)  
DT 30-MAY-2000 (Rel. 39, last annotation update)  
DE Voltage-dependent L-type calcium channel alpha-1D subunit  
DE (CHCAHALD).  
GN CACNA1D  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98070847; PubMed=9405708;  
RA Kollmar R., Montgomery L.G., Fak J., Henry L.J., Hudspeth A.J.;  
RT "Predominance of the alpha1D subunit in L-type voltage-gated Ca<sup>2+</sup>  
RT channels of hair cells in the chicken's cochlea."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:14883-14888(1997).  
[2]  
ALTERNATIVE SPLICING.  
RP MEDLINE=98070848; PubMed=9405709;  
RX Kollmar R., Fak J., Montgomery L.G., Hudspeth A.J.;  
RT "Hair cell-specific splicing of mRNA for the alpha1D subunit of  
RT voltage-gated Ca<sup>2+</sup> channels in the chicken's cochlea."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:14889-14893(1997).  
CC -1- FUNCTION: THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM  
CC CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE  
CC "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP.  
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY (BY  
CC SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: MANY VARIANTS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE BASILAR PAPILLA OF THE  
CC COCHLEA.  
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
CC FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

FT	DOMAIN	5	8	POLY-GLN.
FT	DOMAIN	674	680	POLY-LEU.
FT	DOMAIN	1154	1160	POLY-IIE.
FT	DOMAIN	1703	1706	POLY-GLU.
FT	DOMAIN	424	441	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	359	359	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	726	726	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1122	1122	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1435	1435	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	BINDING	1096	1186	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1449	1515	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	MOD_RES	1461	1504	TO PHENYLALKYLAMINES (BY SIMILARITY).
FT	CA_BIND	1504	1504	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CARBONYL	150	150	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBONYL	324	324	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	VARIABLE	459	484	MISSING (IN ISOFORM I-II-LOOP).
FT	VARIABLE	939	958	ILGADVFYSMTFFELIK -> ILGFEDFAFIAFVEI LK (IN ISOFORM IIIS2).
FT	VARIABLE	1284	1293	MISSING (IN ISOFORM IVS2-IVS3).
FT	VARIABLE	1294	1321	GYPEDAWTFEFLSIGIDVAVLEAD -> HYETDAWNT FDLVAISVDVADIATEVN (IN ISOFORM IVS3).
FT	VARIABLE	1671	1705	AGLTIHGDIGGEIRATISCIDIODEPEENNDEEE -> VL IAHRAQTEPCSPAKLPFGGAEMLDQRAGA (IN CLONE PSE29/31-2).
FT	VARIABLE	1706	2190	MISSING (IN CLONE PSE29/31-2).
FT	VARIABLE	1710	1728	RNGALFGHINHISDRD -> VMSEHGVIYIFLCNNSEFI (IN CLONE PSE29/31-1).
FT	VARIABLE	1729	2190	MISSING (IN CLONE PSE29/31-1).
FT	VARIABLE	1892	1894	HVY -> NGP (IN CLONE PSE48/154-1).
FT	VARIABLE	1893	2190	MISSING (IN CLONE PSE48/154-1).
SO	SEQUENCE	2190 AA;	249342 MW;	10680CICIB7708651 CRC64;
<hr/>				
Query Match				
Best Local Similarity 18.1%; Pred. No. 9.1e-08;				
Matches 95; Conservative 77; Mismatches 164; Indels 188; Gaps 16;				
Oy	16	GGMWPTGVWGRLSELTLGWGDVPVWSCRFCSQQDDGDERERLYFOULPESLSLVLL	75	
Db	330	GGWVPGNGGI-----TDFNFAPAFMLTYFOCI	356	
Oy	76	TTANPDVMIPAYSKNRAYA-----IEFTVTVISLFLMNLTAIIYSQF	121	
Db	357	TWEGMTDVLR--YWWDALGCEMPWITVSLIILTSFPVLNLVLGVLGSERKEBEKAKA	413	
Oy	122	-----RGYL-----MKSIQ	130	
Db	414	RGDPFKLNKKQLLEBDLGMDIMIQAEIDPENDEADEEKRRRVTLADLMEEKKRSR	473	
Oy	131	TSLFERRRLGTAAFEV-----LSSMWEG-----GAPPOATRGPSTS	168	
Db	474	LSCFERSSNKHKSMPTSETESVTNEVSOGENPACCGSLCOTIKSKFSRRMRWRNREN	533	
Oy	169	LRFGRAPSSSSA-----TTTTLTWTGTSAP-NQTWCPRFASCMMOM-CCLLSV	214	
Db	534	RKCKRAANKSVTFEYLVLYVLFNLTLTISSSEHYNOPDMILTQIQDIANKVLLFLFCENKI	593	
Oy	215	MTSWGFSTASSICTTCWCCSRSLPMACEGTCPPATCTLGSSBPLSCWRPEMVGLLSIM	274	
Db	594	KMYSLGLAQFYSLRNREDCFV-----VCGGIVETLVELTELMSPLG-----	635	
Oy	275	DMTRLNLMIYFRFLRIIPSMAPIAVASTYGLVQNARAFGLVVY---YFAIIGI	331	
Db	636	-----ISVFRVRLIRIKFYTRHMWASLSNLVASLSMKSIASLSLLLFLFLIIFSLLGM	690	
Oy	332	NLFRGVIALPENSLSLAPANGSAPCGSFPLETEYMANNPDDFAALVLTLLMNLVNVNMNO-V	390	
Db	691	-----NPNMQRYGSGTDNDPNPOLITDTPDTITDPTITGETDPAWY	731	



QY 391 FLDAVRRYSGPMK-----IYFVLMVLVSVIWNFLALLEN 429  
 Db 732 MYGIMAYGSPSSGMIVCIYIFLITFCGMYILLNVLAVDN 775

RESULT 2  
 CCAC\_RAT STANDARD: PRT: 2169 AA  
 ID CCAC\_RAT P22002: P27733; P27734; Q62816; Q63271; Q64178;  
 AC 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Voltage-dependent L-type calcium channel alpha-1C subunit (calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (RAT  
 DE brain class C) (RBC)  
 GN CACNA1C OR CACNA1A1 OR CCHL1A1 OR CACH2 OR CACN2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN  
 RP SEQUENCE FROM N.A. (CARDIAC ISOFORM S3B).  
 RC TISSUE=Aorta;  
 RX MEDLINE=91009241; PubMed=2170396;  
 RA Koch W.J., Ellinor P.T., Schwartz A.;  
 RT "CDNA cloning of a dihydropyridine-sensitive calcium channel from rat  
 RT aorta. Evidence for the existence of alternatively spliced forms.";  
 RL J. Biol. Chem. 265:17786-17791(1990).  
 RN  
 RP SEQUENCE FROM N.A. (ISOFORMS RBC-I AND RBC-II).  
 RC TISSUE=Brain;  
 RX MEDLINE=91299339; PubMed=1648941;  
 RA Snutch T.P., Tomlinson W.J., Leonard J.P., Gilbert M.M.;  
 RT "Distinct calcium channels are generated by alternative splicing and  
 RT are differentially expressed in the mammalian CNS.";  
 RL Neuron 7:45-57(1991).  
 RN  
 RP SEQUENCE OF 1168-1413 FROM N.A. (CLONE RBC-61).  
 RX MEDLINE=90239020; PubMed=1692134;  
 RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;  
 RT "Rat brain expresses a heterogeneous family of calcium channels.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).  
 RN  
 RP SEQUENCE OF 1269-1415 FROM N.A. (ISOFORMS S3A; S3B AND DELETED D1).  
 RX MEDLINE=92159076; PubMed=1311102;  
 RA Diebold R.J., Koch W.J., Ellinor P.T., Wang J.-J., Mutchamy M.,  
 RA Wiczonek D.F., Schwartz A.;  
 RT "Mutually exclusive exon splicing of the cardiac calcium channel  
 RT at subunit generates developmentally regulated isoforms in the rat  
 RT heart.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1497-1501(1992).  
 RN  
 RP SEQUENCE OF 1269-1387 FROM N.A.  
 RC TISSUE=Myometrium;  
 RX MEDLINE=96043375; PubMed=7485440;  
 RA Tezuka N., Ali M., Chwalisz K., Garfield R.E.;  
 RT "Changes in transcripts encoding calcium channel subunits of rat  
 RT myometrium during pregnancy.";  
 RL Am. J. Physiol. 269:C1008-C1017(1995).  
 RN  
 RP SEQUENCE OF 1202-1495 FROM N.A. (ISOFORM DELETED D1 FORM/ROB2).  
 RC TISSUE=Osteosarcoma;  
 RX MEDLINE=96074617; PubMed=4479909;  
 RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;  
 RT "Multiple calcium channel transcripts in rat osteosarcoma cells:  
 RT selective activation of alpha 1D isoform by parathyroid hormone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).  
 RN  
 RP PHOSPHORYLATION.  
 RX MEDLINE=93374932; PubMed=8396138;  
 RA Hell J.W., Yokoyama C.T., Wong S.T., Warner C., Snutch T.P.,  
 RA Caterall W.A.;

RT "Differential phosphorylation of two size forms of the neuronal class  
 RT C L-type calcium channel alpha 1 subunit.";  
 RL J. Biol. Chem. 268:19451-19457(1993).  
 CC  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C  
 CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)  
 CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)  
 CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP).  
 CC PHENYALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-111A  
 CC (OMEGA-AGA-111A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-  
 CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT  
 CC ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.  
 CC  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC S3A, CARDIAC ADULT ISOFORM S3B (SHOWN HERE), CARDIAC DELETED D1  
 CC FORM/ROB2, BRAIN ISOFORM RBC-I AND BRAIN ISOFORM RBC-II; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC  
 CC -1- TISSUE SPECIFICITY: RBC-I AND RBC-II ARE EXPRESSED THROUGHOUT THE  
 CC CENTRAL NERVOUS SYSTEM, WITH HIGHEST LEVELS IN THE OLFACTORY BULB  
 CC AND CEREBELLUM. ALSO EXPRESSED IN HEART, PITUITARY, ADRENAL GLAND,  
 CC LIVER, KIDNEY, AND IN A MUCH LESSER EXTENT IN TESTES AND SPLEEN.  
 CC  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM EMBRYONIC DAY 16 THROUGH THE  
 CC ADULT.  
 CC  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC  
 CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF  
 CC INHIBITS THE OPENING OF THE CHANNEL (BY SIMILARITY).  
 CC  
 CC -1- PTM: PHOSPHORYLATION BY CAK ACTIVATES THE CHANNEL (PROBABLE). IS  
 CC ALSO PHOSPHORYLATED IN VITRO BY CAM-KINASE II, PKC AND GSKP.  
 CC  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL: M59786; AAA85463.1; -  
 CC EMBL: M67515; AAA18905.1; -  
 CC EMBL: M67516; AAA42016.1; -  
 CC EMBL: M91242; AAA41460.1; -  
 CC EMBL: M91240; AAA41460.1; JOINED.  
 CC EMBL: M89924; AAA41460.1; JOINED.  
 CC EMBL: M91241; AAA41460.1; JOINED.  
 CC EMBL: S80558; AAB35528.1; -  
 CC EMBL: U31815; AAA89157.1; -  
 CC InterPro: IPR002077; Ca\_channel.  
 CC InterPro: IPR002111; Cal\_channel\_TrypL.  
 CC InterPro: IPR000636; Cation\_chan\_non\_lig.  
 CC InterPro: IPR001862; Channel\_pore\_Ca\_Na.  
 CC Pfam: PF00520; Ion\_trans\_4.  
 CC PRINTS: PR00167; CACHANNEL.  
 CC KMW: K01001; Transmembrane; Ion transport; Voltage-gated channel;  
 CC KMW: Calcium channel; Glycoprotein; Repeat; Multigene family;  
 CC KMW: Calcium-binding; Phosphorylation; Alternative splicing.  
 CC FT REPEAT 141 438 1.

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FT REPEAT 540 786 II.
FT REPEAT 917 1198 III.
FT REPEAT 1235 1508 IV.
FT DOMAIN 1 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 173 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 174 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 211 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 212 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 242 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 243 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 281 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 282 300 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 301 320 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 321 410 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 411 435 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 436 554 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 555 573 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 574 588 S2 OF REPEAT II (POTENTIAL).
FT TRANSMEM 589 608 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 609 616 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 617 635 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 636 645 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 646 664 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 665 683 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 684 703 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 704 758 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 759 783 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 784 930 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 931 949 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 950 965 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 966 985 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 986 997 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 998 1016 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1017 1023 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1024 1041 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1042 1060 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1061 1080 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1081 1170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1171 1195 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1196 1248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1249 1267 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1268 1282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1283 1302 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1303 1310 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1311 1329 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1330 1353 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1354 1372 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1373 1391 S6 OF REPEAT IV (POTENTIAL).
FT TRANSMEM 1392 1411 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1412 1480 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1481 1505 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1506 2169 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2169 475 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT DOMAIN 476 630 POLY-LEU.
FT DOMAIN 631 798 POLY-GLU.
FT DOMAIN 799 804 POLY-ILE.
FT DOMAIN 805 1182 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 393 393 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 736 736 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1116 1116 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

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Query Match  
Best Local Similarity 19.3%; Score 196; DB 1; Length 2169;  
Pred. No. 1.9e-07;  
Matches 104; Conservative 83; Mismatches 172; Indels 180; Gaps 22;

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QY 46 CSQDDGQDERLTYFQNPESITSLVLTANNPDVMIPTAKRAYA-----LEFIV 100
DB 362 CKRGWDG-PKHGITNEDNFAFLTFQCTIMGWDVL---YMODAGYELPWVYFS 417
QY 101 FYTIGSLFNLNLTAIIYSF-----RGTL----- 125

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DB 418 LVIFSGFEVLNLVLGVLSGEFSKEREKAKARDFOKLRKQOLEDLKGIDMTIQAEDI 477
QY 126 -----MKSLQTS-----LFRRRLGTRAAEVLSSNVGEGA 156
DB 478 DPENEDEGDEKDPKRMSPHTSETESVNTENVAGGIBEGNCARLAHRISKS-----K 531
QY 157 FPGATRGSTSLRFGCRAPSSSA-----TTLTITWGTSSP-WQWCFACSW 203
DB 532 FSRVWRMRNRFCRRKCAVAVKSNVEFWLVFLVFLNTLITASEHNQPMWLEVDOTAN- 590
QY 204 CWMQKCLISVYMS-----SMGFSASSLCITTCWCCSRSLPNAECGTCPTATCLTG 256
DB 591 -----KALLAFTAEMLKMYSLGLQATVYSLFNRCDCI-----VCGIETIIVERKI 640
QY 257 SSPV--SCWRPEVYGLSLMDTMRMLIVERFLRIIPSKPMNAVASTVLGLVQNMRA 314
DB 641 MSPLGISCMR--CVRLRLRIFKIRYWNST-----SNLVASLINSLSRS 680
QY 315 FGGILVVY---YVPAIIGINLFRGYVALPGNSIAPANGSAPCGSFQOLEYMANNPDD 371
DB 681 IASILLILFLFIIFISLGMQIFGKRF-----NFDEKQTRSTFQDN 721
QY 372 FAALVYTLNMLVYNNM-QVELDAYRRYSGPMCK-----IFYLWMLVSSVIVMLFLAL 425
DB 722 FPGSLVFOILIGEDNSVMTGICATYAGSPFGMLVCIFYILFISPNYILNLFLAI 781
QY 426 ILENFL-----HKMDPRSHLOPLACT--DEATYQMTVELLPDILIEEGDEDLTE 473
DB 782 AVDLMAESLTSQKKEEERKRLATPASPDK-----QEVMEKPAVERSK 831

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RESULT 3  
CCAE\_RAT STANDARD; PRT; 2222 AA.  
AC 007652;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (RBE-II) (RBE2)  
DE (Brain calcium channel II) (BII).  
DE CACNA1E OR CACNA1A6 OR CACNA6.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
RX MEDLINE=93262464; PubMed=8386125;  
RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,  
RA Snutch T.P.;  
RT "Structure and functional expression of a member of the low voltage-activated calcium channel family.";  
RT Science 260:1133-1136(1993).  
RL  
-I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP). OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.  
-I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM





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FT SITE 658 658 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1375 1375 (BY SIMILARITY).
FT SITE 1666 1666 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1666 1666 (BY SIMILARITY).
FT CA_BIND 427 438 BY SIMILARITY.
FT MOD_RES 1737 1737 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CA_BIND 1755 1766 BY SIMILARITY.
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1569 1569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1562 1562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2272 AA; 257233 MW; 70D920B9E0C87A1 CRC64;

Query Match 7.4%; Score 194; DB 1; Length 2272;
Best Local Similarity 20.8%; Pred. No. 2,8e-07;
Matches 113; Conservative 86; Mismatches 221; Indels 122; Gaps 21;

OY 32 LMGDPVWVSCRFCSQDDGDG---RRLTYFQNLPSLTSLLVLTANNPDVMPA 87
DB 260 LMGDPVWVSCRFCSQDDGDG---RRLTYFQNLPSLTSLLVLTANNPDVMPA 87
OY 88 YSKNRYA-----IFPIYTVGSLFLMNLALIALYSQF-----RGYLMKSLQTS 132
DB 317 YTNMDALGATWMLVTFPIPLITIGSFVLNVGLVSGEFAKEREVENRAEFKLRQOQ 376
OY 133 LFRRLGTRA---AFEVL--SSWVEGGAFPQATRGSTSLR--FCRAPSSSATTL 184
DB 377 IREELNGYRAWIDKAEVLAENKNSGTSALEVLRATIKSRTEAMRDSDEHCYDI 436
OY 165 TTWGT---SSPWQWCPFACSCWCMOCCLISV--MISS---WGFSTASSICTTWCSC 234
DB 437 SSVGIPLARASIKSTKVDGASYFRKHEKRLRISIRHMVKSQVYFVTLVSVALNTACVAI 496
OY 235 CSRSIP-WACE-----GTCPTATLUTGSSPSLSCAR-PEMVG 270
DB 497 VHHNQPWHLTHLYAEFLFLCLFLLMSLKMYGMGR---LYRHSNCFDEGVYVS 552
OY 271 L--SLMDMTRM-----LNLIVFRRLRITPSKMPAAVAVSTVLGVQNNRAEGGILVVY 323
DB 553 IFEVVAITRPSTGSGISVLRALRLRIKRYMASLNLVYSLMSKSIISLFLLF 612
OY 324 ---YVFAITIGLFGVIALVGLNGSSLAPANGSAPCGSEGLEEYANNFDDFAALVTIM 380
DB 613 LEIVFVALLGMQLFGGRENFGDTPSA-----NEDTPEALIMTVF 652
OY 381 NLAVVNNV--QVFLDAYRRY---SGPWSKIYFVLMVLYSSVAVNLFALLILENL---- 431
DB 653 QILTGEDNWEVYNGIRSGGVSSGMSAIIYIVLTGNTYLLNLVFLAIVADNANAOE 712
OY 432 -----HKWDPRSHLOPLAGTPREATYQMTVELFRDILPEPGDELTERTLS 476
DB 713 LTKDEEEAEAFNOKHALOKAKEVSPMASPNPSTIERDRRRHHHMSMWRPSHLLRERR 772
OY 477 OH 478
DB 773 RH 774

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## RESULT 5

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CCAE_HUMAN STANDARD: PRT; 2312 AA.
ID CAE_HUMAN Q15878; Q14581; Q14580;
AC Q15878; Q14581; Q14580;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-dependent R-type calcium channel alpha-1B subunit (Calcium
DE channel, L type, alpha-1 polypeptide, isoform 6) (Brain calcium
DE channel II) (B11).
GN CACNA1B OR CACNA1A6 OR CACNA6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA MEDLINE=95236033; PubMed=7536609;
RA Schneider T., Wei X., Olcese R., Costantin J.L., Neely A., Palade P.,
RA Perez-Reyes E., Qin N., Zhou J., Crawford G.D., Smith R.G.,
RA Appel S.H., Stefani E., Birnbaumer M.;
RT "Molecular analysis and functional expression of the human type E
RT neuronal Ca2+ channel alpha 1 subunit.";
RL Recept. Channels 2:255-270(1994).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX MEDLINE=94350992; PubMed=8071363;
RX Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F.,
RX Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
RT "Structure and functional characterization of neuronal alpha 1E
RT calcium channel subtypes.";
RL J. Biol. Chem. 269:22347-22357(1994).
CC - FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA).
CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPIRIDINES (DHP), OMEGA-
CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
CC IMPORTANT FOR INFORMATION PROCESSING.
CC - SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1E-1 AND ALPHA-1E-3
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC - TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES AND IN KIDNEY.
CC - DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC - SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC -----
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CC -----
DR EMBL; L27745; AAA72125.1; -
DR EMBL; L29384; AAA59204.1; -
DR EMBL; L29385; AAA59205.1; -
DR MIM; 601013; -
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Ca_channel_TripL.
DR InterPro; IPR000636; Ca_channel_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CACCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Alternative splicing.

```

FT	REPEAT	76	354	I (BY SIMILARITY).
FT	REPEAT	462	706	II (BY SIMILARITY).
FT	REPEAT	1139	1425	III (BY SIMILARITY).
FT	REPEAT	1462	1725	IV (BY SIMILARITY).
FT	DOMAIN	1	89	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	90	108	S1 OF REPEAT I.
FT	DOMAIN	109	127	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	128	146	S2 OF REPEAT I.
FT	DOMAIN	147	158	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	159	173	S3 OF REPEAT I.
FT	DOMAIN	174	185	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	186	205	S4 OF REPEAT I.
FT	DOMAIN	206	223	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	224	244	S5 OF REPEAT I.
FT	DOMAIN	245	326	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	327	350	S6 OF REPEAT I.
FT	DOMAIN	351	476	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	477	496	S1 OF REPEAT II.
FT	DOMAIN	497	509	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	510	529	S2 OF REPEAT II.
FT	DOMAIN	530	538	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	539	557	S3 OF REPEAT II.
FT	DOMAIN	558	567	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	568	586	S4 OF REPEAT II.
FT	DOMAIN	587	605	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	606	625	S5 OF REPEAT II.
FT	DOMAIN	626	678	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	679	703	S6 OF REPEAT II.
FT	DOMAIN	704	1147	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1148	1164	S1 OF REPEAT III.
FT	DOMAIN	1165	1188	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1189	1208	S2 OF REPEAT III.
FT	DOMAIN	1209	1216	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1217	1239	S3 OF REPEAT III.
FT	DOMAIN	1240	1253	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1254	1271	S4 OF REPEAT III.
FT	DOMAIN	1272	1290	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1291	1310	S5 OF REPEAT III.
FT	DOMAIN	1311	1397	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1398	1421	S6 OF REPEAT III.
FT	DOMAIN	1422	1478	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1479	1497	S1 OF REPEAT IV.
FT	DOMAIN	1498	1512	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1513	1532	S2 OF REPEAT IV.
FT	DOMAIN	1533	1540	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1541	1559	S3 OF REPEAT IV.
FT	DOMAIN	1560	1570	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1571	1589	S4 OF REPEAT IV.
FT	DOMAIN	1590	1608	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1609	1628	S5 OF REPEAT IV.
FT	DOMAIN	1629	1697	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1698	1723	S6 OF REPEAT IV.
FT	DOMAIN	1724	2312	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	716	721	POLY-GLU.
FT	DOMAIN	748	753	POLY-ARG.
FT	TRANSMEM	767	772	POLY-VAL.
FT	DOMAIN	1227	1230	POLY-ARG.
FT	TRANSMEM	2283	2287	POLY-ARG.
FT	DOMAIN	374	391	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	309	309	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	657	657	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1371	1371	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1662	1662	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CA_BIND	426	437	BY SIMILARITY.
FT	MOD_RES	1733	1733	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1751	1762	BY SIMILARITY.
FT	CARBOND	254	254	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOND	1365	1365	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CABOHAYD	1570	1570	N-LINKED (GELCNC. . .) (POTENTIAL).		
FT	VASPPHYD	748	766	MISSING (IN ISOFORM ALPHA-1E-1).		
FT	CONFLICT	648	648	I -> M (IN REF. 2).		
FT	CONFLICT	836	837	WP -> IAL (IN REF. 2).		
FT	CONFLICT	1954	1954	T -> A (IN REF. 2).		
FT	CONFLICT	1966	2008	MISSING (IN REF. 2).		
FT	CONFLICT	2076	2076	R -> P (IN REF. 2).		
FT	CONFLICT	2083	2083	G -> R (IN REF. 2).		
FT	CONFLICT	2205	2205	C -> W (IN REF. 2).		
FT	CONFLICT	2218	2218	S -> R (IN REF. 2).		
FT	CONFLICT	2244	2244	G -> V (IN REF. 2).		
SO	SEQUENCE	2312 AA; 261727 MM; 633BD3EFDA07D65E CRC64;				
Query Match 7.3%, Score 191; DB 1; Length 2312;						
Best Local Similarity 19.4%; Pred. No. 4.9e-07;						
Matches 106; Conservative 91; Mismatches 218; Indels 132; Gaps 20						
QY	32	LMGGRPVVWPSRFGSCQDDGDG	-----RRLRFGNLPESTSLVLTLTANNPDVMPDA	87		
DB	259	LEGFDPHPCGVGCGPAGCECKDKMTGPNDDGTQFDNILEFVLTVRQCITMEGTTVL	-----	315		
QY	88	YSKNAYV	-----LFFVFTVIGSLFNLNLAIITYSP	-----RGYLSLQTS 132		
DB	316	YNTNDALGATNMWLTFLPIIIGSEFVLTVLGVLSGEFAKERERENRAEMKLRRQOQ	-----	375		
QY	133	LFRRRLGTRAAEVLSSWVGEGGAPQARRRGPRSTSLRCRAPSSSATTTLTWGTS	-----	192		
DB	376	IERELNGRAWIDKAEVW	-----IAEENKAGTSLLEVLRATTKIRSKRTETAMTRDSD	430		
QY	193	W	-----QTMCPFACS	-----MCMOMCCILSY	-----WTSS	-----WGFSTASSLCT 229
DB	431	HCVDSSVGTPLARRSISAKAKVDGVSYPFHKKRLLRISIRHNWKSQVFWYIVLSVALNT	-----	490		
QY	230	TCWSCCSNLP	WACE	-----GTCTPATCLTGSSPLSCWR	P	265
DB	491	ACVAIVHHNQPWLTHLYAEFLGLFLLEMSLKMVMGPR	-----	LYFHSSEFCEDG 546		
QY	266	EWVGLL	-----SLMOMTRY	-----LNMLIVFRFLIIESMKPMAYASVTLGYVMRAFGI	318	
DB	547	VYVGSIFEEVYVAFIRPGTSFGISVLRALRLNIFKTKWASLRNLYVLSMSKSIISL	-----	606		
QY	319	LVVYV	-----VYFAIIGINLEFRGVIVALPGNSSLPANGSAPCGSEOLEYANNFDDPAA	375		
DB	607	LELLELFVIFVALLGQLEFGRENFNDGPSSA	-----	NEDFPAA 646		
QY	376	LVTLNNLWVNNM	-----OVELDAYRRY	-----SGPMSKIYFVLMVLSSYIVNLFTALILENF	430	
DB	647	ITVFOIILGEPHNEVMTYGTIRSGGVSSGMSAIFYLVLTLEFGNTLLNVLFAIVDNL	-----	706		
QY	431	I	-----HKWDPRSHLOPLAGTEPATYQMTVELLFRDIEPEDEBL	471		
DB	707	ANAQETKDEQEEEAFNOKHALOKAEKSPMSGAPNMPISIERDRRRRHHSWMEPRSSH	-----	766		
QY	472	TERLSOH	478			
DB	767	RERRRRH	773			
RESULT 6						
CCAD_MESAU STANDARD; PRT; 1610 AA.						
AC	099244; 099245;					
DT	15-JUL-1999 (Rel. 38, Created)					
DT	15-JUL-1999 (Rel. 38, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha1 polypeptide isoform 2).					
DE	CACNAID OR CACNL1A2 OR CCHL1A2 OR CAC3 OR CACNA.					
OS	Eucaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;					
NCBI_TaxID=10036;						

RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM HCA3A).  
 RC TISSUE=Insulinoma;  
 RX MEDLINE=93149124; PubMed=1337146;  
 RA Yancy G.C., Wheeler M.B., Wei X., Perez-Reyes E., Birnbaumer L.,  
 RT Boyd A.E. III, Moss L.G.;  
 RT "Cloning of a novel alpha 1-subunit of the voltage-dependent calcium  
 channel from the beta-cell";  
 RL Mol. Endocrinol. 6:2143-2152(1992).  
 RN [2]  
 RP SEQUENCE OF 1146-1441 FROM N.A. (ISOFORMS CAC3B AND CAC3D).  
 RC TISSUE=Heart;  
 RX MEDLINE=91056091; PubMed=2173707;  
 RA Perez-Reyes E., Wei X., Castellano A., Birnbaumer L.;  
 RT "Molecular diversity of L-type calcium channels. Evidence for  
 alternative splicing of the transcripts of three non-allelic genes";  
 RL J. Biol. Chem. 265:20430-20436(1990).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-ID  
 GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)  
 CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)  
 GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),  
 PHENYALKALAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-ITIA  
 (OMEGA-AGA-ITIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-  
 GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FOR-  
 MING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; HCA3A (SHOWN HERE),  
 CAC3B AND CAC3D; ARE PRODUCED BY ALTERNATIVE SPLICING. CAC3B  
 IS IDENTICAL TO HCA3A IN THE FRAGMENT SEQUENCED.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART AND SKELETAL MUSCLE.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M57969; AAB59702.1; -;  
 DR EMBL; M57970; AAB62807.1; -;  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR002111; Cat\_channel\_TrpL.  
 DR InterPro: IPR000636; CatIon\_chan\_non\_lig.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans; 4.  
 DR PRINTS; PR00167; CACCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Alternative splicing.  
 FT REPEAT 112 408  
 FT REPEAT 508 754  
 FT REPEAT 871 1153  
 FT REPEAT 1190 1465  
 FT DOMAIN 1 125  
 FT TRANSMEM 126 144  
 FT CYTOPLASMIC (POTENTIAL).  
 FT SI OF REPEAT I (POTENTIAL).

FT	DOMAIN	145	162	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	163	182	S2 OF REPEAT I (POTENTIAL).
FT	DOMAIN	183	194	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	195	213	S3 OF REPEAT I (POTENTIAL).
FT	DOMAIN	214	234	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	235	253	S4 OF REPEAT I (POTENTIAL).
FT	DOMAIN	254	272	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	273	292	S5 OF REPEAT I (POTENTIAL).
FT	DOMAIN	293	380	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	381	405	S6 OF REPEAT I (POTENTIAL).
FT	DOMAIN	406	522	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	523	542	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	543	557	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	558	576	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	577	584	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	585	603	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	604	613	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	614	632	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	633	651	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	652	672	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	673	726	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	727	751	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	752	884	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	885	903	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	904	919	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	920	939	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	940	951	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	952	970	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	971	976	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	977	996	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	997	1015	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1016	1035	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1036	1125	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1126	1146	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1147	1203	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1204	1222	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1223	1237	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1238	1257	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1258	1264	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1265	1286	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1287	1311	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1312	1331	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1332	1350	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1351	1370	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1371	1437	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1438	1462	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1463	1610	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1	6	POLY-MET.
FT	DOMAIN	652	658	POLY-LEU.
FT	TRANSMEM	826	836	POLY-GLU.
FT	DOMAIN	428	445	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	363	363	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	704	704	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1099	1099	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1404	1404	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	BINDING	1073	1163	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1418	1484	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	1430	1473	TO PHENYALKALAMINES (BY SIMILARITY).
FT	MOD_RES	1473	1473	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1491	1502	POTENTIAL.
FT	CARBOHYD	154	154	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	224	224	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	VARSPLIC	1261	1303	GFSDAMNFTSLVIGSITIVASEADPESGSLPPTAT PG->HYFTDAMNFTFDALIVGSAVDIAITFEVN (IN ISOFORM CAC3D).
FT	SEQUENCE	1610 AA;	182327 MM;	B3B3E3794D936F79 CRC64;







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FT TRANSMEM 1464 1483 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1484 1491 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1492 1510 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1511 1519 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1520 1538 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1539 1557 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1558 1577 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1578 1638 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1639 1663 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1664 2223 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 40 POLY-ALA.
FT DOMAIN 729 735 POLY-SER.
FT DOMAIN 1064 1068 POLY-GLU.
FT DOMAIN 386 403 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT SITE 321 321 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 671 671 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1323 1323 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 1611 1611 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT CA_BIND 439 450 BY SIMILARITY.
FT MOD_RES 1674 1674 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CA_BIND 1692 1703 BY SIMILARITY.
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1300 1300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1519 1519 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2223 AA: 251827 MW: 59722DC03E1CFC5B CRC64:

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Query Match 7.2%; Score 189.5; DB 1: Length 2223;  
 Best Local Similarity 19.9%; Pred. No. 6.2e-07;  
 Matches 107; Conservative 87; Mismatches 197; Indels 147; Gaps 25;

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QY 43 CRFGSGDDGQDRKRYTFQNLPSLSLVLTANNPDWITPKSNRRAVA-----IF 97
DB 291 CSYWGPNPDG-----ITQFDNLFLALTLVFCITMEGWTTLI---YNTDDALGAMWNMLY 342
QY 98 FIVEFVIGSLFLMNLTLITISQF-----RGYLMKSLQTSIFRRRLGTRA-----A 143
DB 343 FIPILITISFVNLVGLVGEFAKEREVENRNSFLKLRQOOIERELNGYRAMIDKA 402
QY 144 FEVL---SSWVGEGGAPQATRRG--PSTSLRFGCRAPSSSATTTTLTWTGSSP----- 192
DB 403 EEVMLEENKKNAGEKSAI-HYLRRATIKKRRMIEQTESSEDOYTEISSVG--SPLARAS 459
QY 193 -----W-----QWCFPACSW---CMNQ 207
DB 460 IKSTKLEGSSTFRKREMLRISIRHMKSHAFTYIVLGLVALNTVCVAVHYDQPLMLS 519
QY 208 MCCLISVTSSMGESTASSLCTTCWCSCSRSLPMACEGTCPTPATCLTGGSPSLCWR--PE 266
DB 520 NPLVAAETFLGIPS--SEMFLKMYGCGPR-----LTFHSSFNFDGCV 561
QY 267 MVGLL--SLMDTRM-----LNMILVFRLRITPSMKPMVAVASTVLGVQNMRAFGITL 319
DB 562 IIGSFDFVWVTLIREPSTFGISVIALRLRLRIFKTKTWASIRNLVYLSMSKMSITISL 621
QY 320 VVVV---VVFALIGINIRGVIALPGNSSLAPANGSAPCGSEFDELEWANNPDFPAAL 376
DB 622 FLFLFLVIFVFLDGLQGLGG-----QNFEEGTPP-----TNDFEPAAI 661
QY 377 VTLNMLVNVNM--QVFLDAYRRY---SGPMKIFVLMVLISSYIWNLFALILENFL 431
DB 662 ITVFQILGEDMNEVNYMGISQGGVNSGMSSVYFIVLTLEFNGTTLNLFALIAVDNIA 721
QY 432 HKMPDRSLQPLAGTPPEATYQVVELLRDT--LEPGEDELTERLSQHPH--LMLCR 485
DB 722 NAOELTKEEOE---EEEAINKHALOKRAKESVPMSPAGPFPSTERERRRHKHMSIWEAR 776

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RESULT 8

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CCAF_HUMAN
ID CCAF_HUMAN STANDARD: PRT: 1966 AA.
AC 060840: 043901:
DT 15-0UL-1999 (Rel. 38, Created)
DT 15-0UL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1f subunit.
GN CACNA1F OR CACNA1F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS CSN2 D-369; Q-508; W-1049 AND
RP H-1364.
RC TISSUE=Retina.
RX MEDLINE=98324776; PubMed=9662399;
RA Strom T.M., Nyakatura G., Apfelstedt-Sylla E., Hellebrand H.,
RA Lorenz B., Weber B.H.F., Wutz K., Gutwillinger N., Ruether K.,
RA Drescher B., Sauer C., Zrenner E., Meitinger T., Rosenthal A.,
RA Meindl A.;
RT "An L-type calcium channel gene mutated in incomplete X-linked
RT congenital stationary night blindness.";
RL Nat. Genet. 19:260-263(1998).
[2]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U.,
RA Meindl A., Rosenthal A.;
RL Submitted (Feb-2000) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE OF 1200-1966 FROM N.A.
RX MEDLINE=9808923; PubMed=9344658;
RA Fisher S.E., Ciccodicola A., Tanaka K., Curci A., Desicato S.,
RA D'Urso M., Craig I.W.;
RT "Sequence-based exon prediction around the synaptophysin locus reveals
RT a gene-rich area containing novel genes in human proximal Xp.";
RL Genomics 45:340-347(1997).
-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
CC PHENYLTALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-IIIA
CC (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSION IN SKELETAL MUSCLE AND RETINA.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- DISEASE: DEFECTS IN CACNA1F ARE CAUSES OF INCOMPLETE X-LINKED
CC CONGENITAL STATIONARY NIGHT BLINDNESS (CSN2), A NONPROGRESSIVE
CC RETINAL DISORDER CHARACTERIZED BY DECREASED VISUAL ACUTY AND LOSS
CC OF NIGHT VISION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
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DR EMBL: AJ006216; CAA06916.1; -  
 DR EMBL: AJ224874; CAA12175.1; -  
 DR EMBL: AF235097; AAF62518.1; -  
 DR EMBL: U93305; AAB92359.1; -  
 DR MIM: 300110; -  
 DR MIM: 300071; -  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR002111; Cat\_channel\_TrpL.  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans; 4.  
 DR PRINTS: PRO0167; CACHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Disease mutation; Vision.

FT REPEAT 79 375 I.  
 FT REPEAT 504 750 II.  
 FT REPEAT 847 1129 III.  
 FT REPEAT 1166 1433 IV.  
 FT DOMAIN 1 92 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 93 111 S1 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 112 129 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 130 149 S2 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 150 161 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 162 180 S3 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 181 201 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 202 220 S4 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 221 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 259 S5 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 260 347 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 348 372 S6 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 373 518 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 519 538 S1 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 539 553 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 554 572 S2 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 573 580 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 581 599 S3 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 600 609 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 610 628 S4 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 629 647 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 648 668 S5 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 669 722 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 723 747 S6 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 748 860 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 861 879 S1 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 880 895 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 896 915 S2 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 916 927 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 928 946 S3 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 947 952 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 953 972 S4 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 973 991 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 992 1011 S5 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1012 1101 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1102 1122 S6 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1123 1179 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1180 1198 S1 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1199 1213 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1214 1233 S2 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1234 1240 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1241 1262 S3 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1263 1279 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1280 1299 S4 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1300 1318 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1319 1338 S5 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1339 1405 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1406 1430 S6 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1431 1966 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 648 654 POLY-LEU.

FT DOMAIN 783 788 POLY-GLU.  
 FT DOMAIN 798 814 POLY-GLU.  
 FT DOMAIN 1110 1113 POLY-ILE.  
 FT DOMAIN 1629 1634 POLY-GLU.  
 FT DOMAIN 395 412 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).  
 FT SITE 330 330 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 700 700 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1075 1075 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1372 1372 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT BINDING 1049 1139 TO DIHYDROPYRIDINES (BY SIMILARITY).  
 FT BINDING 1386 1452 TO DIHYDROPYRIDINES (BY SIMILARITY).  
 FT BINDING 1398 1441 TO PHENYLALKYLAMINES (BY SIMILARITY).  
 FT MOD\_RES 1441 1441 PHOSPHORYLATION (BY CARK) (POTENTIAL).  
 FT CA\_BIND 1459 1470 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 295 295 G->D (IN CSNB2).  
 FT VARIANT 369 369 /Ftd=VAR.001504.  
 FT VARIANT 508 508 R->Q (IN CSNB2).  
 FT VARIANT 1049 1049 /Ftd=VAR.001505.  
 FT VARIANT 1049 1049 R->W (IN CSNB2).  
 FT VARIANT 1364 1364 /Ftd=VAR.001506.  
 FT CONFLICT 1225 1225 L->H (IN CSNB2).  
 FT CONFLICT 1265 1271 E->V (IN REF. 3).  
 FT CONFLICT 1652 1767 MISSING (IN REF. 3).  
 FT CONFLICT 1849 1849 A->G (IN REF. 3).  
 SO SEQUENCE 1966 AA; 219494 MW; FEB47E19FA57E3D CRC64;

Query Match 7.1%; Score 187.5; DB 1; Length 1966;  
 Best Local Similarity 18.6%; Pred. No 7.8e-07;  
 Matches 101; Conservative 73; Mismatches 169; Indels 199; Gaps 20;

QY 4 ACWEATGRCRLGGGMVPTGVRGLELSLWGGDPVWPCSCSQDDGDDRRERYFQ 63  
 DB 291 ACTLNOTBCR--GRMPGNGGI-----TNDN 315

QY 64 LPESLTSLLVLTTRANNDDVMIPAYSKNRAYA-----IFVFVTVGSLPLMLTLTIY 118  
 DB 316 FFFAALTVFCVTEGWGTDVL--YMDAMGYELPWYEVSLVFFSPVLNLVLGLVS 372

QY 119 SQF-----RGYLNKSIO-----TSL 133  
 DB 373 GEFSEKREKAKARGDFOKREKQOMEDLRGYLDWITQAEELDMEDPSADONLGPOLAE 432

QY 134 FRRRLG-----TRAPEVLS-----SNV-----GEGAPQATR----- 162  
 DB 433 TNRRTGRRLRWFESHSTSHSTSHASLSPASDTGSMTEQDEDEEGALASCFLCKLM 492

QY 163 -----RGSTSLRF--CRAPSSSA-----TTTLTWGTSPPQOTWCFACSW 203  
 DB 493 KTRCGRRLRRANRYARACRAVKSNAQYAVLLVFLNLTITLASEHIGOPWLTOIQEX 552

QY 204 CWMQCCLLSY--MTSSWGFSTASLCT-----TCWSSCSRLPWACEGTCPPATCI 256  
 DB 553 ANKVLLCFLYEMLLKLKLGAPSAVSSFFNRFCFVCG-----GILETTLVEGA 604

QY 257 SSPLSWCRPEWVGLISLDMTRMLNLVFERLRIIFSKPMVAVSTVGLVONMRAFG 316  
 DB 605 MQLG-----ISVLRCAVLLRIFVYTRHMASLNLVASLNSMKSIA 646

QY 317 GLIVVY---YFPAIGINIFRGIVVALPGNSSLAPANGSAPCGSFQOLEYMANPEDFA 373  
 DB 647 SLLLLFLFLITIFSLGQLFGKRF-----NFDQTHKSTFTFPP 687

QY 374 AALVTLMKLVNVMNQVFL--DAYRRYSQPMK-----YFVLMVLSSVIVNLFLLIL 427  
 DB 688 QALITVPIILIGEDMNVMYMGIMAYGGFFPPGALVCIYFIILFCNGIILANVFLAI 747

QY 428 EN 429  
Db 748 DN 749

RESULT 9  
CCAD\_HUMAN STANDARD: PRT; 2161 AA.  
ID CCAD\_HUMAN 001668; Q13916; Q13931;  
AC 15-JUL-1999 (Rel. 38, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 2).  
GN CACNA1D OR CACNA1A2 OR CCHLA2 OR CACH3 OR CACNA4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (NEURONAL-TYPE ISOFORM).  
RC TISSUE-Neuroblastoma;  
RX MEDLINE=92110010; PubMed=1309651;  
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelcbl G., Ellis S.B., Harpold M.M.;  
RT "Structure and functional expression of alpha1, alpha2, and beta subunits of a novel human neuronal calcium channel subtype.";  
RL Neuron 8:71-84(1992).  
RN [2]  
RP SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM).  
RC TISSUE-Pancreatic Islets;  
RX MEDLINE=92115705; PubMed=130948;  
RA Seino S., Chen L., Seino M., Blondel O., Takeda J., Johnson J.H., Bell G.I.;  
RT "Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expressed in pancreatic beta cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:584-588(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (BETA-CELL-TYPE ISOFORM), AND VARIANT NIDDM.  
RX MEDLINE=96044438; PubMed=7557998;  
RA Yamada Y., Masuda K., Li Q., Ihara Y., Kubota A., Miura T., Nakamura K., Fujii Y., Seino S., Seino Y.;  
RT "The structures of the human calcium channel alpha 1 subunit (CACNA1A2) and beta subunit (CACNB3) genes.";  
RL Genomics 27:312-319(1995).  
RN [4]  
RP FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
RN [5]  
RP SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
RN [6]  
RP SUBCELLULAR LOCATION: Integral membrane protein.  
RN [7]  
RP ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; NEURONAL-TYPE (SHOWN HERE) AND BETA-CELL-TYPE, ARE PRODUCED BY ALTERNATIVE SPLICING.  
RN [8]  
RP TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN, WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.  
RN [9]  
RP DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS

CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -1- POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT ARG TRINUCLEOTIDE  
CC REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS  
CC BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES  
CC MELLITUS (NIDDM).  
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
CC FAMILY.  
CC -----  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; M76558; AAA58402.1; -;  
CC EMBL; M83566; AAA35629.1; -;  
CC EMBL; D43747; BAA07804.1; -;  
CC EMBL; D43705; BAA07804.1; JOINED.  
CC EMBL; D43706; BAA07804.1; JOINED.  
CC EMBL; D43707; BAA07804.1; JOINED.  
CC EMBL; D43708; BAA07804.1; JOINED.  
CC EMBL; D43709; BAA07804.1; JOINED.  
CC EMBL; D43710; BAA07804.1; JOINED.  
CC EMBL; D43711; BAA07804.1; JOINED.  
CC EMBL; D43712; BAA07804.1; JOINED.  
CC EMBL; D43713; BAA07804.1; JOINED.  
CC EMBL; D43714; BAA07804.1; JOINED.  
CC EMBL; D43715; BAA07804.1; JOINED.  
CC EMBL; D43716; BAA07804.1; JOINED.  
CC EMBL; D43717; BAA07804.1; JOINED.  
CC EMBL; D43718; BAA07804.1; JOINED.  
CC EMBL; D43719; BAA07804.1; JOINED.  
CC EMBL; D43720; BAA07804.1; JOINED.  
CC EMBL; D43721; BAA07804.1; JOINED.  
CC EMBL; D43722; BAA07804.1; JOINED.  
CC EMBL; D43723; BAA07804.1; JOINED.  
CC EMBL; D43724; BAA07804.1; JOINED.  
CC EMBL; D43725; BAA07804.1; JOINED.  
CC EMBL; D43726; BAA07804.1; JOINED.  
CC EMBL; D43727; BAA07804.1; JOINED.  
CC EMBL; D43728; BAA07804.1; JOINED.  
CC EMBL; D43729; BAA07804.1; JOINED.  
CC EMBL; D43730; BAA07804.1; JOINED.  
CC EMBL; D43731; BAA07804.1; JOINED.  
CC EMBL; D43732; BAA07804.1; JOINED.  
CC EMBL; D43733; BAA07804.1; JOINED.  
CC EMBL; D43734; BAA07804.1; JOINED.  
CC EMBL; D43735; BAA07804.1; JOINED.  
CC EMBL; D43736; BAA07804.1; JOINED.  
CC EMBL; D43737; BAA07804.1; JOINED.  
CC EMBL; D43738; BAA07804.1; JOINED.  
CC EMBL; D43739; BAA07804.1; JOINED.  
CC EMBL; D43740; BAA07804.1; JOINED.  
CC EMBL; D43741; BAA07804.1; JOINED.  
CC EMBL; D43742; BAA07804.1; JOINED.  
CC EMBL; D43743; BAA07804.1; JOINED.  
CC EMBL; D43744; BAA07804.1; JOINED.  
CC EMBL; D43745; BAA07804.1; JOINED.  
CC EMBL; D43746; BAA07804.1; JOINED.  
CC MIM; 114206; -;  
CC InterPro; IPR002077; Ca\_channel.  
CC InterPro; IPR002111; Cat\_channel\_trpl.  
CC InterPro; IPR000636; Cation\_chan\_non\_lig.  
CC InterPro; IPR001682; Channel\_pore\_Ca\_Na.  
CC Pfam; PF00520; ion\_trans\_4.  
CC PRINTS; PR00167; CACHANNEL.  
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
CC Calcium channel; Glycoprotein; Repeat; Multigene family;  
CC Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;  
CC Triplet repeat expansion.

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FT REPEAT 113 409 I.
FT REPEAT 509 755 II.
FT REPEAT 873 1155 III.
FT REPEAT 1192 1467 IV.
FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 127 145 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 164 183 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 164 195 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 196 214 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 215 235 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 236 254 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 255 273 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 274 293 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 294 381 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 382 406 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 407 523 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 524 543 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 544 558 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 559 577 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 578 585 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 586 604 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 605 614 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 615 633 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 634 652 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 653 673 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 674 727 S6 OF REPEAT II (POTENTIAL).
FT TRANSSEM 728 752 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 753 886 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 887 905 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 906 921 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 922 941 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 942 953 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 954 972 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 973 978 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 979 998 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 999 1017 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1018 1037 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1038 1127 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1128 1148 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1149 1205 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1206 1224 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1225 1239 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1240 1259 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1260 1266 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1267 1288 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1289 1313 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1314 1333 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1334 1352 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1353 1372 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1373 1439 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1440 1464 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1465 2161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1 7 POLY-MET.
FT DOMAIN 653 659 POLY-LEU.
FT TRANSSEM 827 838 POLY-GLU.
FT DOMAIN 429 446 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT SITE 364 364 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT SITE 705 705 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

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Query Match 7.1%; Score 187; DB 1; Length 2161;  
 Best Local Similarity 18.5%; Pred. No. 9.4e-07;  
 Matches 94; Conservative 81; Mismatches 157; Indels 176; Gaps 20;

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OY 12 CRLGSGMVPVWYRGLESLMGSDPVVWMSCRCSQDDGQDEKRTLYQNPELSL 71
DB 333 CR--SGWVGNGI-----TNDNFAFALTY 357
OY 72 LVLLTANPDVMTDAVSKNRAYA-----IPFIVFVIGSLFLNLLTALTIYSQFRGYLM 126

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DB 358 FOCITMEGWTDVL---YWMNDAMGFELPNVYFVSLVFGSPFVLNLVLGLVSGEFSKERE 414
OY 127 KSLQTSLEFRRRLGTRAFEVYLSMVG-----EGG-----APF----- 158
DB 415 KAKARGDQKREKQQLBEDLKGVLDTQAEIDPDNEBEGGEKGRNMTSTSESV 474
OY 159 -----QATRGSTSLRFCRAPSSSATTTLTWGTSSPWOTWCF-----AC 201
DB 475 NTEVSGEGEGRGCGSL--COALSKSK-----LSRRWRNRNRRRCRAAVKSV 523
OY 202 SWCMWMOCL-LSVMTSS-----WGF-----STASSLCTTCMSC-----CSRSLP--- 240
DB 524 TFYMLVLYVLVNLTLISSEHYNOPDMLTQIDIANVLLALFCEMLVMTSLGLDAYF 563
OY 241 -----WACGTCTPATCTLGSSPLSCWBPENYGLLSLMDTRMLMLVFERFLR 290
DB 564 VSLRFRCFCFVCGGITETILVELEINSPG-----ISVFCVALLR 625
OY 291 IIPSKPAAVVAAYSLVLQNMRAFGILVYV---YVPAIIGINLFRGVYALPGNSL 347
DB 626 IFKVTFRHTSLCNLVASILNSKSSASILLFLFIIIFSLGMLGGRF----- 676
OY 348 APANSAACGSEFQLEVMANNEPDAALVTLMLLVYNNMO-VFLDAYRRYSGPMK-- 404
DB 677 -----NDETQTKRSTFDNPPQALTVFQILGEDMNAVYGINAYGCGPSSSGM 726
OY 405 ---YFVLMVLVSSVYVNLFLALLEN 429
DB 727 IVCIFITLFCGNVILLNVLATAVDN 754

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RESULT 10  
 ID CCAE\_RABIT STANDARD; PRT; 2259 AA.  
 AC 002343; 002344;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Voltage-dependent R-type calcium channel alpha-1E subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 6) (Brain calcium channel II) (BII).  
 DE CACNA1E OR CACNA1A6 OR CACNA6.  
 GN Oryctolagus cuniculus (Rabbit).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=92354772; PubMed=1379552;  
 RA Nidome T., Kim M.S., Friedrich T., Mori Y.;  
 RT "Molecular cloning and characterization of a novel calcium channel from rabbit brain.";  
 RT FEBS Lett. 308:7-13(1992).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-ACATOXIN-IIA (OMEGA-AGA-IIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA

CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BIT-1 (SHOWN HERE) AND BIT-2;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE CEREBRAL CORTEX, HIPPOCAMPUS,  
 CC AND CORPUS STRIATUM.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X67855; CA448040.1; -  
 DR EMBL: X67856; CA448041.1; -  
 DR PIR: S29236; S29236.  
 DR PIR: S29237; S29237.  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR002111; Cat\_channel\_Tryp.  
 DR InterPro: IPR000636; Cation\_chan\_non\_lig.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans\_4.  
 DR PRINTS: PR00167; CACHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Alternative splicing.  
 FT REPEAT 76 354 I.  
 FT REPEAT 76 706 II.  
 FT REPEAT 1130 1414 III.  
 FT REPEAT 1453 1716 IV.  
 FT DOMAIN 1 89 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 90 108 S1 OF REPEAT I.  
 FT DOMAIN 109 126 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 127 146 S2 OF REPEAT I.  
 FT DOMAIN 147 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 176 S3 OF REPEAT I.  
 FT DOMAIN 177 185 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 186 204 S4 OF REPEAT I.  
 FT DOMAIN 205 223 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 224 243 S5 OF REPEAT I.  
 FT DOMAIN 244 326 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 327 351 S6 OF REPEAT I.  
 FT DOMAIN 352 476 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 477 495 S1 OF REPEAT II.  
 FT DOMAIN 496 510 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 511 530 S2 OF REPEAT II.  
 FT DOMAIN 531 538 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 539 557 S3 OF REPEAT II.  
 FT DOMAIN 558 567 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 568 586 S4 OF REPEAT II.  
 FT DOMAIN 587 605 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 606 625 S5 OF REPEAT II.  
 FT DOMAIN 626 678 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 679 703 S6 OF REPEAT II.  
 FT DOMAIN 704 1143 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1144 1162 S1 OF REPEAT III.  
 FT DOMAIN 1163 1178 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1179 1198 S2 OF REPEAT III.  
 FT DOMAIN 1199 1210 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1211 1229 S3 OF REPEAT III.  
 FT DOMAIN 1230 1243 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1244 1262 S4 OF REPEAT III.  
 FT DOMAIN 1263 1281 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1282 1301 S5 OF REPEAT III.

FT	DOMAIN	1302	1388	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1389	1413	S6 OF REPEAT III.
FT	DOMAIN	1414	1468	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1469	1487	S1 OF REPEAT IV.
FT	DOMAIN	1488	1502	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1503	1522	S2 OF REPEAT IV.
FT	DOMAIN	1523	1530	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1531	1549	S3 OF REPEAT IV.
FT	DOMAIN	1550	1561	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1562	1580	S4 OF REPEAT IV.
FT	DOMAIN	1581	1599	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1600	1619	S5 OF REPEAT IV.
FT	DOMAIN	1620	1688	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1689	1712	S6 OF REPEAT IV.
FT	DOMAIN	1713	2259	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1716	721	POLY-GLU.
FT	DOMAIN	748	753	POLY-ARG.
FT	TRANSMEM	767	772	POLY-ARG.
FT	DOMAIN	1218	1221	POLY-VAL.
FT	TRANSMEM	1976	1979	POLY-SER.
FT	DOMAIN	2231	2235	POLY-ARG.
FT	TRANSMEM	374	391	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	DOMAIN	309	309	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	TRANSMEM	657	657	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	DOMAIN	1362	1362	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	TRANSMEM	1653	1653	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	DOMAIN	426	437	MOD.RES
FT	TRANSMEM	1724	1724	CA_BIND
FT	DOMAIN	1742	1753	CARBOHYD
FT	TRANSMEM	254	254	CARBOHYD
FT	DOMAIN	1556	1556	CARBOHYD
FT	TRANSMEM	1561	1561	VARSPLIC
FT	DOMAIN	2101	2259	

SEQUENCE 2259 AA; 254250 MW; E4A75707638779E CRC64;

Query Match 7.1%; Score 187; DB 1; Length 2259;  
 Best Local Similarity 18.1%; Pred. No. 9.9e-07;  
 Matches 102; Conservative 91; Mismatches 207; Indels 162; Gaps 18;

QY	32	LMGGDPVYVWMSRCFGSQDQDGD	---RRLTYFQNLPESTLSLVLLTTANNPDWIRA	87	
DB	259	LEGFDPHPCGVGCGAGTECKDWIGPNDGITQFDNLFAVLVFOCTIMEGTVLL	---	315	
QY	88	YSKNRAYA	-----IPFIVTVIGSLFIMNLTAIYSQF	-----RGYLMKSLQTS	132
DB	316	YMTNALGATWMTWLYTIPILIIISFEVLMVLVGLSGEFAKERERYENRAFAKLRRQO	375		
QY	133	LRRRLRGTAAREVYLSMYGEGGAFQATRRGPSTLSRCRAPSSSATTTLTWTGSSP	192		
DB	376	IERELMGYRAMIDKAEVM	-----LAENKNGSTALEVLRATIKRSRTTEATRDSSD	429	
QY	193	WQTCWCFACSWCMQMCCLSVWTS	-----	218	
DB	430	-----EHCVDIISVGTPLAASIKSAVDASVFRHRELLRISVRAVVS	475		
QY	219	---WGFSTASSLCTTCWSCCSRLP	-----GTCPTPA	251	
DB	476	QVFYVIVLSLVALNACVAIVHNNQPMFLTHLLYAEFLGLFLEMSLKMGMKPR	---	533	
QY	252	TCLTGSPLSCMR-PEMWGLL	---SLMDKTRM	---	303
DB	534	---LYFHSSFNCFDFGVTGSIIEVVAIRPQTSFGISVLRALRLRLRIKIRKYNASLRN	591		



CC EMBL: X05921; CAA29355.1; -  
 DR EMBL: M23919; AAA31159.1; -  
 DR PIR: A30063; A30063.  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR002111; Cat\_channel\_TrpL.  
 DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans\_4.  
 DR PRINTS: PR00167; CACHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Polymorphism.  
 FT REPEAT 38 337  
 FT REPEAT 418 664  
 FT REPEAT 786 1068  
 FT REPEAT 1105 1384  
 FT DOMAIN 1 51  
 FT TRANSMEM 52 70  
 FT DOMAIN 71 88  
 FT TRANSMEM 89 108  
 FT DOMAIN 109 120  
 FT TRANSMEM 121 139  
 FT DOMAIN 140 160  
 FT TRANSMEM 161 179  
 FT DOMAIN 180 198  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 309  
 FT TRANSMEM 310 334  
 FT DOMAIN 335 342  
 FT TRANSMEM 433 451  
 FT DOMAIN 452 466  
 FT TRANSMEM 467 486  
 FT DOMAIN 487 494  
 FT TRANSMEM 495 513  
 FT DOMAIN 514 523  
 FT TRANSMEM 524 542  
 FT DOMAIN 543 561  
 FT TRANSMEM 562 581  
 FT DOMAIN 582 636  
 FT TRANSMEM 637 661  
 FT DOMAIN 662 799  
 FT TRANSMEM 800 818  
 FT DOMAIN 819 834  
 FT TRANSMEM 835 854  
 FT DOMAIN 855 866  
 FT TRANSMEM 867 885  
 FT DOMAIN 886 892  
 FT TRANSMEM 893 911  
 FT DOMAIN 912 930  
 FT TRANSMEM 931 950  
 FT DOMAIN 951 1040  
 FT TRANSMEM 1041 1065  
 FT DOMAIN 1066 1118  
 FT TRANSMEM 1119 1137  
 FT DOMAIN 1138 1152  
 FT TRANSMEM 1153 1172  
 FT DOMAIN 1173 1180  
 FT TRANSMEM 1181 1199  
 FT DOMAIN 1200 1231  
 FT TRANSMEM 1232 1250  
 FT DOMAIN 1251 1269  
 FT TRANSMEM 1270 1289  
 FT DOMAIN 1290 1356  
 FT TRANSMEM 1357 1381  
 FT DOMAIN 1382 1873  
 FT TRANSMEM 357 374  
 FT DOMAIN 562 568  
 FT SITE 292 292  
 FT SITE 614 614  
 FT SITE 1014 1014

-----  
 S1 OF REPEAT I (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S2 OF REPEAT I (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S3 OF REPEAT I (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S4 OF REPEAT I (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S5 OF REPEAT I (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S6 OF REPEAT I (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S1 OF REPEAT II (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S2 OF REPEAT II (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S3 OF REPEAT II (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S4 OF REPEAT II (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S5 OF REPEAT II (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S6 OF REPEAT II (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S1 OF REPEAT III (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S2 OF REPEAT III (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S3 OF REPEAT III (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S4 OF REPEAT III (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S5 OF REPEAT III (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S6 OF REPEAT III (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S1 OF REPEAT IV (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S2 OF REPEAT IV (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S3 OF REPEAT IV (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S4 OF REPEAT IV (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 S5 OF REPEAT IV (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 S6 OF REPEAT IV (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 BINDING TO THE BETA SUBUNIT.  
 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).

FT (BY SIMILARITY).  
 Query Match 7.1%; Score 186; DB 1; Length 1873;  
 Best Local Similarity 18.1%; Pred. No. 9,7e-07;  
 Matches 94; Conservative 81; Mismatches 166; Indels 178; Gaps 19;  
 QY 58 LTVFQNLPESTLSLVLTANNPDVMI PAVSKRAYA-----IEFTVTVYIGSLFLML 112  
 Db 272 ITHFDNFGFSLVYQGITMGMTDVL---YVNDAGNEMPIYFTLLIGSFFIINTL 328  
 QY 113 LTAITYQFQGYLMLKSLQTSIFRRRLGTRAFVLYLSMVG----- 152  
 Db 329 VLGLSEFTRKERRKASRGTFQRLREKQLEEDREGVMSWITGVEYVDLEKGLSL 388  
 QY 153 -EGGAFPOATR--RGFSTSLFCRAPASSSATTLTWTGTSPPQWTW---CPFACS--- 202  
 Db 389 EEGSDTESLEYELGKLKTIQFIR-----HMRQNRVFRMKCHLYK 430  
 QY 203 ---WCMQMC-----CLLSVMT-----SSWGFSTAS 225  
 Db 431 SRVFWVLVILVALNTLSIASEHNQPLMLTHQDIANRVLSFTIEMLLKMYGLRQ 490  
 QY 226 SLCT-----TCWCCSRLP-WACEGICPPATCTLTSSPLSCRPKREYGLSLMDTRM 279  
 Db 491 YFMSIFNRFDFVVCGLLELLVSESGAMP---LGISVLR----- 529  
 QY 280 LNMILVFRFLRITSMKPMAYVASTVGLVQNMRAFGLIIVVY---YFAIIGINLFRG 336  
 Db 530 -----IRLRLFKITKWTSLSNVSLNLSIASLSLTLLEFLITIFLLDMQLFG 583  
 QY 337 VIVALPGNSLAPANGAPCGSPQLEWMANFDDFAALVTLNLMVYNNM-OVFLDAY 395  
 Db 584 RY-----DFEDTEVRSNFDFNPQALISVFQVLGEDMNSVMYGI 624  
 QY 396 RRYGPMK-----IYEVLMVLVSVIWNLFLLILENPLH-----KMDPRSHL 440  
 Db 625 MAYGSPGYVGLVYCIFFILVCGNYTLINVLAIADNLEASLSAQAKAEKRRR 684  
 QY 441 QPLAGTPPATVQMTVELLFRDLEPGEDELTERLSQHP 479  
 Db 685 KMSRGLPKT-----EERKSVAKKLEQKP 709  
 RESULT 12  
 CCAS\_HUMAN STANDARD; PRT; 1873 AA.  
 AC Q13696; Q13934; Q12896;  
 DT 15-JUL-1999 (Rel. 38, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Voltage-dependent L-type calcium channel alpha-1s subunit (Calcium  
 channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle).  
 GN CACNA1S OR CACNA1A3 OR CACNA1 OR CACNA1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=95229168; PubMed=7713519;  
 RA Hogan K., Powers P.A., Gregg R.G.;  
 RT "Cloning of the human skeletal muscle alpha 1 subunit of the  
 RT dihydropyridine-sensitive L-type calcium channel (CACNA1A3).";  
 RL Genomics 24:608-609(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96435439; PubMed=8838325;  
 RA Hogan K., Gregg R.G., Powers P.A.;  
 RT "The structure of the gene encoding the human skeletal muscle alpha 1  
 RT subunit of the dihydropyridine-sensitive L-type calcium channel  
 RT (CACNA1A3).";  
 RL Genomics 31:392-394(1996).



[3] SEQUENCE OF 1200-1300 FROM N.A., AND VARIANTS HYPOKPP GLY-1239 AND  
HIS-1239.  
MEDLINE=94273190; PubMed=8004673;  
RA Placsek L.J., Tawil R., Griggs R.C., Engel A.G., Layzer R.B.,  
RA Kielesni H., McManis P.G., Santiago L., Moore M., Fouad G.,  
RA Bradley F., Leppert M.F.;  
RT "dihydropyridine receptor mutations cause hypokalemic periodic  
paralysis.";  
RL Cell 77:863-868(1994).  
[4]  
SEQUENCE OF 1223-1413 FROM N.A.  
RA Soldator N.M.;  
RT "human skeletal muscle L-type Ca2+ channel alpha 1S subunit gene shows  
splitting patterns similar to alpha 1C and alpha 1D genes in the region  
involved in hereditary disorders.";  
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE OF 788-830: 1019-1085 AND 1293-1318 FROM N.A.  
RX MEDLINE=93162636; PubMed=7916735;  
RA Gregg R.G., Couch F., Hogan K., Powers P.A.;  
RT "Assignment of the human gene for the alpha-1 subunit of the skeletal  
muscle DHP-sensitive calcium channel (CACNL1A3) to chromosome 1q31-  
q32.";  
RT Genomics 15:107-112(1993).  
[6]  
VARIANT HYPOKPP HIS-528.  
RX MEDLINE=95078851; PubMed=7987325;  
RA Jurkat-Rott K., Lehmann-Horn F., Elbaz A., Heine R., Gregg R.G.,  
RA Hogan K., Powers P.A., Lapie P., Vale-Santos J.E., Weissenbach J.,  
RA Fontaine B.;  
RT "A calcium channel mutation causing hypokalemic periodic paralysis.";  
RL Hum. Mol. Genet. 3:1415-1419(1994).  
[7]  
REVISIONS, VARIANT MSH5 HIS-1086, AND VARIANTS HIS-458 AND CYS-1539.  
RX MEDLINE=97342905; PubMed=9199552;  
RA Monnier N., Procaccio V., Stieglitz P., Lunardi J.;  
RT "Malignant-hyperthermia susceptibility is associated with a mutation  
of the alpha-1-subunit of the human dihydropyridine-sensitive L-type  
voltage-dependent calcium-channel receptor in skeletal muscle.";  
RL Am. J. Hum. Genet. 60:1316-1325(1997).  
-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S  
GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)  
CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)  
GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),  
PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-111A  
(OMEGA-AGA-111A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-  
GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT  
ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.  
-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN  
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE  
CHANNEL.  
-1- SUBCELLULAR LOCATION: Integral membrane protein.  
-1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.  
-1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S4, S5, S6) AND ONE  
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
-1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE  
RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE  
FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.

CC -1- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL  
CC FUNCTION (BY SIMILARITY).  
CC -1- DISEASE: DEFECTS IN CACNL1A3 ARE THE CAUSE OF HYPOKALEMIC PERIODIC  
CC PARALYSIS (HYPOKPP OR HOPR1), AN AUTOSOMAL DOMINANT SKELETAL  
CC MUSCLE DISORDER MANIFESTED BY EPISODIC WEAKNESS ASSOCIATED WITH  
CC LOW SERUM POTASSIUM. MUSCLE WEAKNESS COULD BE DUE TO ALTERED  
CC EXCITATION-CONTRACTION COUPLING IN HYPOKPP PATIENTS.  
CC -1- DISEASE: DEFECTS IN CACNL1A3 ARE THE CAUSE OF MALIGNANT  
CC HYPERHERMIA SUSCEPTIBILITY 5 (MHSS); AN AUTOSOMAL DOMINANT  
CC DISORDER THAT IS POTENTIALLY LETHAL IN SUSCEPTIBLE INDIVIDUALS ON  
CC EXPOSURE TO COMMONLY USED INHALANT ANESTHETICS AND  
CC DEPOLARIZING MUSCLE RELAXANTS.  
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: U30707; AAB37235.1; JOINED.  
DR EMBL: U30666; AAB37235.1; JOINED.  
DR EMBL: U30667; AAB37235.1; JOINED.  
DR EMBL: U30668; AAB37235.1; JOINED.  
DR EMBL: U30669; AAB37235.1; JOINED.  
DR EMBL: U30670; AAB37235.1; JOINED.  
DR EMBL: U30671; AAB37235.1; JOINED.  
DR EMBL: U30672; AAB37235.1; JOINED.  
DR EMBL: U30673; AAB37235.1; JOINED.  
DR EMBL: U30674; AAB37235.1; JOINED.  
DR EMBL: U30675; AAB37235.1; JOINED.  
DR EMBL: U30676; AAB37235.1; JOINED.  
DR EMBL: U30677; AAB37235.1; JOINED.  
DR EMBL: U30678; AAB37235.1; JOINED.  
DR EMBL: U30679; AAB37235.1; JOINED.  
DR EMBL: U30680; AAB37235.1; JOINED.  
DR EMBL: U30681; AAB37235.1; JOINED.  
DR EMBL: U30682; AAB37235.1; JOINED.  
DR EMBL: U30683; AAB37235.1; JOINED.  
DR EMBL: U30684; AAB37235.1; JOINED.  
DR EMBL: U30685; AAB37235.1; JOINED.  
DR EMBL: U30686; AAB37235.1; JOINED.  
DR EMBL: U30687; AAB37235.1; JOINED.  
DR EMBL: U30688; AAB37235.1; JOINED.  
DR EMBL: U30689; AAB37235.1; JOINED.  
DR EMBL: U30690; AAB37235.1; JOINED.  
DR EMBL: U30691; AAB37235.1; JOINED.  
DR EMBL: U30692; AAB37235.1; JOINED.  
DR EMBL: U30693; AAB37235.1; JOINED.  
DR EMBL: U30694; AAB37235.1; JOINED.  
DR EMBL: U30695; AAB37235.1; JOINED.  
DR EMBL: U30696; AAB37235.1; JOINED.  
DR EMBL: U30697; AAB37235.1; JOINED.  
DR EMBL: U30698; AAB37235.1; JOINED.  
DR EMBL: U30699; AAB37235.1; JOINED.  
DR EMBL: U30700; AAB37235.1; JOINED.  
DR EMBL: U30701; AAB37235.1; JOINED.  
DR EMBL: U30702; AAB37235.1; JOINED.  
DR EMBL: U30703; AAB37235.1; JOINED.  
DR EMBL: U30704; AAB37235.1; JOINED.  
DR EMBL: U30705; AAB37235.1; JOINED.  
DR EMBL: U30706; AAB37235.1; JOINED.  
DR EMBL: U30707; AAB37235.1; JOINED.  
DR EMBL: U09784; AAA20531.1; -  
DR EMBL: Z50091; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: Z50092; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: Z50093; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: M87486; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: M87487; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: M87488; -; NOT\_ANNOTATED\_CDS.



DR MIM; 114208; -  
 DR MIM; 170400; -  
 DR MIM; 601887; -  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR002111; Ca\_channel\_TrpL.  
 DR InterPro: IPR000636; Cation\_chan\_non\_119.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans\_4.  
 DR PRINTS: PR00167; CACHANNEL.  
 KM Ionic channel: Transmembrane.  
 KM Calcium channel: Glycoprotein, Repeat, Multigene family;  
 FT Calcium binding; Phosphorylation; Disease mutation; Polymorphism.  
 FT REPEAT 38 337 I.  
 FT REPEAT 418 664 II.  
 FT REPEAT 786 1068 III.  
 FT REPEAT 1105 1384 IV.  
 FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 52 70 S1 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 71 88 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 89 108 S2 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 109 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 121 139 S3 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 140 160 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 161 179 S4 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 180 198 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 199 218 S5 OF REPEAT I (POTENTIAL).

Query Match 7.0%; Score 184; DB 1; Length 1873;  
 Best Local Similarity 18.6%; Pred. No. 1.4e-06;  
 Matches 95; Conservative 82; Mismatches 171; Indels 164; Gaps 19;

OY 58 LTFYONLPESLTLVLTANNPDVIMPAYSKNRAVA-----IPFIVTVIGSLFIMNL 112  
 DB 272 ITHFNFGFSMLTVYOCITMEGMTDVL---YWNDAIGNEMPMYVTVITLLIGSEFIINL 328  
 OY 113 LFAIISQPRGLIMKSLQSLFRRLGRTAAFEVLSMWG----- 152  
 DB 329 VLGVLSEGTREKAKSGTFOKLEKQDDEDLRGVSMITQGVMDVEDEFREGKLSL 388  
 OY 153 EGGAFOATRR--GPSTSLRCPAPSSSATTTLTWTSSPMQW---CPFACS----- 202  
 DB 369 DEGSDDTESLYEIAGLKIQPIR-----HWKQNRIFPKKCHDIYK 430  
 OY 203 -----WCWQMCCLLSVMTSS-----W-----GFSTASLCTT----- 230  
 DB 431 SKVEFWILVILVLTLSIASEHNQPLMLTRLODIANRVLLSFTTEKLMKMYGLGRLQ 490  
 OY 221 -----CWSGCSRSRP-WACGTCPTPATCITGSSPLSCWRPEMVGILSLMDTRM 279  
 DB 491 YFMSIFNRPDCVFCVSGILEILLVESGAMTP---LGISVLRC----- 529  
 OY 280 LMLIVFRLRIIPMKPMAVAVSTVLGIYONMRAFGGLVVVY---YVFATIGINLFRG 336  
 DB 530 -----ILRLRFKTKTKWTLSNIVASLINSRISASILLFLFYFALIGMQLEGG 583  
 OY 337 VIVALPGNSSIAPANGAPCGSEFQLEWANNFDDPAALVTLMLIMLVNNN-QVFLDAY 395  
 DB 584 RV-----DFEDTEVRSNFDNFPOALLISVFOVLGEDTSMYNGNI 624  
 OY 396 RRYSGPMWK-----TYFVLMVLVSSVIVNLFALILEFLKMPRSLQLOPLAGTPEAT 450  
 DB 635 MAYGSPSPGMILVCYITFIFLFCGVYILLNVFLAIVADNL-----AEASLTSQAKK 677  
 OY 451 YQMTVELLFRDLEEGDE--LTERLSQHP 479  
 DB 678 AEKKRRKMSKGLPDKSEKSTMAKKLEQRP 709

RESULT 13

CCAC\_HUMAN STANDARD; PRT; 2221 AA.  
 AC Q13936; Q09245; Q09241; Q13917; Q13922; Q13919; Q13920; Q13921;  
 AC Q13924; Q13925; Q13926; Q13927; Q13928; Q13930; Q13918; Q13929;

AC Q13923; Q13933; Q13932; Q15877; Q99875; Q14744; Q14743;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Voltage-dependent L-type calcium channel alpha-1c subunit (Calcium  
 channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle).  
 GN CACNA1C OR CACNL1A1 OR CCHL1A1 OR CACH2 OR CACN2.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM HFCC), AND ALTERNATIVE SPLICING.  
 RC TISSUE=Fetal fibroblast;  
 RA MEDLINE=92262493; PubMed=1316612;  
 RT Soldatov N.M.;  
 RT "Molecular diversity of L-type Ca2+ channel transcripts in human  
 RT fibroblasts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4628-4632(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (HFCC; NEURONAL ISOFORMS H66-2; H2.05 AND H54).  
 RC TISSUE=Lung fibroblast, and Hippocampus;  
 RA MEDLINE=95048396; PubMed=7959794;  
 RX Soldatov N.M.;  
 RT "Genomic structure of human L-type Ca2+ channel.";  
 RL Genomics 22:77-87(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.  
 RC TISSUE=Fibroblast;  
 RA MEDLINE=95256214; PubMed=7737988;  
 RX Soldatov N.M., Bouron A., Reuter H.;  
 RT "Different voltage-dependent inhibition by dihydropyridines of human  
 RT Ca2+ channel splice variants.";  
 RL J. Biol. Chem. 270:10540-10543(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RA Soldatov N.;  
 RT "Functional expression of splice variants of human L-type calcium  
 RT channel (isoform 1 gene).";  
 RL Submitted (JUN-1994) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Hippocampus;  
 RA MEDLINE=97166207; PubMed=9013606;  
 RX Soldatov N.M., Zuelke R.D., Bouron A., Reuter H.;  
 RT "Molecular structures involved in L-type calcium channel  
 RT inactivation.";  
 RL J. Biol. Chem. 272:3560-3566(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS HHT-1; HH05 AND HH06).  
 RC TISSUE=Heart;  
 RA MEDLINE=93317655; PubMed=8392192;  
 RX Schultz D., Mikala G., Yatani A., Engle D.B., Iles D.E., Segers B.,  
 RA Sline R.J., Weghuis D.O., Kloeckner U., Wakamori M., Wang J.-J.,  
 RA Melvin D., Varadi G., Schwartz A.;  
 RT "Cloning, chromosomal localization, and functional expression of the  
 RT alpha1 subunit of the L-type voltage-dependent calcium channel from  
 RT normal human heart.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6228-6232(1993).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORMS HT-1 AND HT-2), AND ALTERNATIVE SPLICING.  
 RC TISSUE=Heart;  
 RA MEDLINE=97242615; PubMed=9087614;  
 RX Kloeckner U., Mikala G., Eisfeld J., Iles D.E., Strobeck M.,  
 RA Mershon J.L., Schwartz A., Varadi G.;  
 RT "Properties of three COOH-terminal splice variants of a human cardiac  
 RT L-type Ca2+-channel alpha1-subunit.";  
 RL Am. J. Physiol. 272:H1372-H1381(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORMS A1C-105 AND A1C-106).  
 RA Soldatov N.M.;  
 RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 RN [9]

RP SEQUENCE OF 1182-1503 FROM N.A. (ISOFORMS CACH2A; CACH2C AND CACH2D).  
 RC TISSUE-Heart; PubMed-2173707;  
 RA MEDLINE-91056091; PubMed-2173707;  
 RA Perez-Reyes E., Wei X., Castellano A., Birnbaumer L.;  
 RT "Molecular diversity of L-type calcium channels. Evidence for  
 RT alternative splicing of the transcripts of three non-allelic genes.";  
 RL J. Biol. Chem. 265:20430-20436(1990).  
 RN [10]  
 RP SEQUENCE OF 1140-1206 FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE-91363396; PubMed-1653763;  
 RA Powers P.A., Gregg R.G., Talley P.A., Liao M., Hogan K.;  
 RT "Assignment of the human gene for the alpha 1 subunit of the cardiac  
 RT DHP-sensitive Ca2+ channel (CCH1A1) to chromosome 12p12-pter.";  
 RL Genomics 10:835-839(1991).  
 RN [11]  
 RP SEQUENCE OF 1196-1421 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-93122776; PubMed-1335957;  
 RA Sun W., McPherson J.D., Hoang D.Q., Wasmuth J.J., Evans G.A.,  
 RA Montal M.;  
 RT "Mapping of a human brain voltage-gated calcium channel to human  
 RT chromosome 12p13-pter.";  
 RL Genomics 14:1092-1094(1992).  
 RN [12]  
 RP MUTAGENESIS AND CALCIUM BINDING.  
 RX MEDLINE-93293809; PubMed-8099908;  
 RA Tang S., Mikala G., Bahinski A., Yatanai A., Varadi G., Schwartz A.;  
 RT "Molecular localization of ion selectivity sites within the pore of a  
 RT human L-type cardiac calcium channel.";  
 RL J. Biol. Chem. 268:13026-13029(1993).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C  
 CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)  
 CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)  
 CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),  
 CC PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-ACETOXIN-ITIA  
 CC (OMEGA-AGA-ITIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-  
 CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT  
 CC ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL ISOMERMS ARE CREATED BY ALTERNATIVE  
 CC SPLICING EVENTS, WHICH SEEM TO OCCUR IN A TISSUE-SPECIFIC MANNER.  
 CC ALL THESE SPLICED VARIANTS PROBABLY COMPOSE CHANNELS WITH DIFFERENT  
 CC GATING PROPERTIES, AND DISPLAY MARKED DIFFERENCES IN THE  
 CC SENSITIVITY TO DHP COMPOUNDS. THE FIBROBLAST ISOMER HFCO IS SHOWN  
 CC HERE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, OVARY, PANCREATIC BETA-  
 CC CELLS AND IN THE BRAIN.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF  
 CC INHIBITS THE OPENING OF THE CHANNEL (BY STIMULANT).  
 CC -1- PTM: PHOSPHORYLATION BY CAPK ACTIVATES THE CHANNEL (BY  
 CC STIMULANT).  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
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[illegible]

RESULT 14	
CCAB_RABIT	
ID CCAB_RABIT	STANDARD;
NO COSIEC	PRT; 2339 AA

CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE  
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B  
CC GIVES RISE TO "N-TYPE" CALCIUM CURRENTS. "N-TYPE" CALCIUM CHANNELS  
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED  
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CITX-GVIA) AND BY OMEGA-AEATOXIN-  
CC IIA (OMEGA-AAGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO  
CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AAGA-IVA).  
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN  
CC DIRECTED MIGRATION OF IMMATURE NEURONS.

CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.

CC -1- HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.

CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK

CC	(BY SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; D14157; BAA03202.1; -	
DR	InterPro; IPR002077; Ca_channel.	
DR	InterPro; IPR002111; Cat_channel_Tryp.	
DR	InterPro; IPR000636; Cation_chan_non_11g.	
DR	InterPro; IPR001682; Channel_pore_Ca_Na.	
DR	Pfam; PF00520; Ion_trans; 4.	
KW	PRINTS; PR00167; CACCHANNEL.	
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;	
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;	
KW	Calcium-binding; Phosphorylation; ATP-binding.	
FT	REPEAT	82
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FT	DOMAIN	1687

TRANSMEM 1687 1711 S6 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1712 2339 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 2051 2055 POLY-HIS.  
 FT DOMAIN 2119 2123 POLY-SER.  
 FT DOMAIN 2319 2324 POLY-GLY.  
 FT DOMAIN 379 396 BINDING TO THE BETA SUBUNIT (BY  
 SIMILARITY).  
 FT NP\_BIND 452 459 ATP (POTENTIAL).  
 FT SITE 314 314 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 FT SITE 663 663 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 FT SITE 1370 1370 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 FT SITE 1658 1658 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 (BY SIMILARITY).  
 FT MOD\_RES 1722 1722 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT CA\_BIND 1740 1751 BY SIMILARITY.  
 FT CARBOHYD 1256 1256 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 1566 1566 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 1678 1678 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 2339 AA; 261178 MW; 0413DA93794C8B34 CRC64;

Query Match 6.9%; Score 182; DB 1; Length 2339;  
 Best Local Similarity 19.3%; Pred. No. 2.5e-06;  
 Matches 107; Conservative 87; Mismatches 166; Indels 194; Gaps 23;

36 DPVVPWSC-----RFGSQDGDGDR-----RLTYQNLPELSLVLITRANND 82  
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 83 VMLPAVSKNRVA-----JFFIVFVIGSLFNLNLTAITYSQF----- 121  
 319 IL--YNTNDAAGNTWMLTIFILLIIGTFMNLVGLVLSGFARERVENRAFLK 375  
 122 -----RGYL-----MKSLSQSLFERRICTRAAEVLSMWG 152  
 376 RROQIIRERLNGYLEWIFKAEVYMLAEEDRNAEKSPLAVLKRRAAKSRSDILOAEBG 435  
 153 EGGAFFPATRRGPSTSLRFRAPSSSATTLTWTGSSP-----WOTMCPF-----A 200  
 436 EG-----RLTGLCAGSPPARASLSGKTESSYRRKREKMFIRRMVRA 482  
 201 CSMCMOMCCLLSVMTSSMGSTASSLCTTCWSSCNSLP-----WACESTCPT 249  
 483 QSEFWYVLCV-----ALNTLCVAMVHYNQORLTALYFAEFVFLGLEFL 528  
 250 PATC-LTGSSPLSCWPE-----WGLL--SLMDMTM-----LNMLIVRFLRIIP 293  
 529 EMSLKMVGLGPRSYFRSSFCDEGVTVGSIFEVYMAAVRPGTSFGISVLRLRLRITK 588  
 294 SMKEMAVAVSTVLGIVONMRAFGIILVYV--YVFAIIGINLFRGIVTALPGNSSIAPA 350  
 589 VTKWNSIRNLVLSMSKSIITLLEFLFLFYVFAILLMOLEFGQGF----- 636  
 351 NGAPCSFEQLEXYMANFEDFAALVTLNMLVYNNMVOFLDAYRIS-----GPMIS 403  
 637 -----NFKD-ETPTNFDEFPAILITVFOILGEDMVM--YHIESOGGVSRGMS 666  
 404 KIIVYLMVLSVIVMNLFLAILLENFLHKMDPRSHQPLAGPEATYQMTVELFRDIL 463  
 687 SFYFVILTFEGNYTLNLAIVADN-----LANOELT----- 720  
 464 EEPGEDELTERLSQ 477  
 721 --KDEEMEAANQ 732

RESULT 15  
 CCAC\_RABIT STANDARD: PRT: 2171 AA.  
 ID CCAC\_RABIT P15381: 099243; Q28676; 003716;  
 DT 01-Apr-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE voltage-dependent L-type calcium channel alpha-1C subunit (Calcium  
 DE channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle).  
 DE (Smooth muscle calcium channel blocker receptor) (CACB-receptor).  
 GN CACNA1C OR CACNA1L1 OR CCHL1L1 OR CACH2 OR CACNA2.  
 OC Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE=8930539; PubMed=2474130;  
 RA Mikami A., Imoto K., Tanabe T., Ni Idoume T., Mori Y., Takeshima H.,  
 RA Narumaya S., Numa S.;  
 RT "Primary structure and functional expression of the cardiac  
 RT dihydropyridine-sensitive calcium channel.";  
 RL Nature 340:230-233(1989).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart, and Lung;  
 RX MEDLINE=90382589; PubMed=2169433;  
 RA Biel M., Ruth P., Bosse E., Hüllin R., Stuehmer W., Flockerzi V.,  
 RA Hofmann F.;  
 RT "Primary structure and functional expression of a high voltage  
 RT activated calcium channel from rabbit lung.";  
 RL FEBS Lett. 269:409-412(1990).  
 RN [3]  
 RP SEQUENCE OF 1-98 FROM N.A. (CLONE 141).  
 RC TISSUE-Heart muscle;  
 RX Biel M., Hüllin R., Freundner S., Singer D., Dascal N., Flockerzi V.,  
 RA Hofmann F.;  
 RT "Tissue specific expression of high voltage activated dihydropyridine  
 RT sensitive L-type calcium channels.";  
 RL submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1192-1485 FROM N.A. (ISOFORM CACH2C).  
 RC TISSUE-Heart;  
 RX MEDLINE=91056091; PubMed=2173707;  
 RA Perez-Reyes E., Wei X., Castellano A., Birnbaumer L.;  
 RT "Molecular diversity of L-type calcium channels. Evidence for  
 RT alternative splicing of the transcripts of three non-allelic genes.";  
 RL J. Biol. Chem. 265:20430-20436(1990).  
 RN [5]  
 RP MUTAGENESIS, AND CALCIUM BINDING.  
 RX MEDLINE=94050141; PubMed=8232554;  
 RA Yang J., Ellinor P.T., Sather W.A., Zhang J.-F., Tsien R.W.;  
 RT "Molecular determinants of Ca2+ selectivity and ion permeation in  
 RT L-type Ca2+ channels.";  
 RL Nature 366:158-161(1993).  
 RN [6]  
 RP MUTAGENESIS OF CYS-168.  
 RX MEDLINE=98171540; PubMed=9502794;  
 RA Ren D., Xu H., Eberl D.F., Chopra M., Hall L.M.;  
 RT "A mutation affecting dihydropyridine-sensitive current levels and  
 RT activation kinetics in Drosophila muscle and mammalian heart calcium  
 RT channels.";  
 RL J. Neurosci. 18:2335-2341(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY CAPK.  
 RX MEDLINE=92387386; PubMed=1325377;  
 RA Yoshida A., Takahashi M., Nishimura S., Takeshima H., Kokubun S.;  
 RT "Cyclic AMP-dependent phosphorylation and regulation of the cardiac  
 RT dihydropyridine-sensitive Ca channel.";  
 RL FEBS Lett. 309:343-349(1992).  
 RN [8]  
 RP BETA-SUBUNIT BINDING DOMAIN.  
 RX MEDLINE=94150724; PubMed=7509046;  
 RA Praegerelli K.P., de Waard M., Mori Y., Tanabe T., Snutch T.P.,  
 RA Campbell K.P.;  
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II  
 RT cytoplasmic linker of the alpha 1-subunit.";

RL Nature 368:67-70(1994).

RN [9]

RP EF-HAND MOTIF AND CALCIUM INACTIVATION.

RA MEDLINE-96095215; PubMed-7491499.

RA de Leon M., Wang Y., Jones L., Perez-Reyes E., Wei X., Soong T.W.,

RT Snutch T.P., Yue D.T.,

RT "essential Ca(2+) binding motif for Ca(2+)-sensitive inactivation of

RT L-type Ca2+ channels."

RL Science 270:1502-1505(1995).

CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE

CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED

CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE

CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,

CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1C

CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)

CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)

CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),

CC PHENYLAALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-III

CC (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-

CC GYIA (OMEGA-CTX-GYIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).

CC CALCIUM CHANNELS CONTAINING THE ALPHA-1C SUBUNIT PLAY AN IMPORTANT

CC ROLE IN EXCITATION-CONTRACTION COUPLING IN THE HEART.

CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT

CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-

CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS

CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM

CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA

CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; THE HEART ISOFORMS

CC CAC2A (SHOWN HERE), CAC2C, CAC2D AND A LONG ISOFORM, ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: EXPRESSION IN CARDIAC MUSCLE. IN LUNG,

CC EXPRESSED IN AIRWAY AND VASCULAR SMOOTH MUSCLE CELLS.

CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE

CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE

CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS

CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A

CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- DOMAIN: BINDING OF INTRACELLULAR CALCIUM THROUGH THE EF-HAND MOTIF

CC INHIBITS THE OPENING OF THE CHANNEL.

CC -1- PTM: PHOSPHORYLATION BY CAK ACTIVATES THE CHANNEL.

CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS

CC FAMILY.

CC -----

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CC -----

DR EMBL: X15539; CA33546.1; -

DR EMBL: X55763; CA39289.1; -

DR EMBL: M57974; AA31182.1; -

DR EMBL: X60782; CA43196.1; -

DR PIR: S05054; S05054.

DR InterPro: IPR002077; Ca\_channel.

DR InterPro: IPR002111; Cal\_channel\_Tryp.

DR InterPro: IPR000636; Calion\_chan\_non\_11g.

DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.

DR Pfam: PF00520; Ion\_trans; 4.

DR PRINTS: PR00167; CACCHANNEL.

KM Ionic channel, Transmembrane; Ion transport; Voltage-gated channel;

KW Calcium channel; Glycoprotein; Repeat; Multigene family;

KW Calcium-binding; Phosphorylation; Alternative splicing.

FT REPEAT 141 438 I.

FT REPEAT 540 786 II.

FT REPEAT 917 1199 III.

FT REPEAT 1236 1509 IV.

FT DOMAIN 1 154 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	155	173	S1 OF REPEAT I.
FT	DOMAIN	174	190	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	191	211	S2 OF REPEAT I.
FT	DOMAIN	212	223	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	224	242	S3 OF REPEAT I.
FT	DOMAIN	243	262	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	263	281	S4 OF REPEAT I.
FT	DOMAIN	282	300	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	301	320	S5 OF REPEAT I.
FT	DOMAIN	321	410	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	411	435	S6 OF REPEAT I.
FT	DOMAIN	436	554	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	555	573	S1 OF REPEAT II.
FT	DOMAIN	574	588	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	589	608	S2 OF REPEAT II.
FT	DOMAIN	609	616	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	617	635	S3 OF REPEAT II.
FT	DOMAIN	636	645	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	646	664	S4 OF REPEAT II.
FT	DOMAIN	665	683	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	684	703	S5 OF REPEAT II.
FT	DOMAIN	704	758	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	759	783	S6 OF REPEAT II.
FT	DOMAIN	784	930	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	931	949	S1 OF REPEAT III.
FT	DOMAIN	950	965	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	966	985	S2 OF REPEAT III.
FT	DOMAIN	986	997	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	998	1016	S3 OF REPEAT III.
FT	DOMAIN	1017	1023	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1024	1042	S4 OF REPEAT III.
FT	DOMAIN	1043	1061	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1062	1081	S5 OF REPEAT III.
FT	DOMAIN	1082	1171	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1172	1196	S6 OF REPEAT III.
FT	DOMAIN	1197	1249	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1250	1268	S1 OF REPEAT IV.
FT	DOMAIN	1269	1283	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1284	1303	S2 OF REPEAT IV.
FT	DOMAIN	1304	1311	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1312	1330	S3 OF REPEAT IV.
FT	DOMAIN	1331	1354	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1355	1373	S4 OF REPEAT IV.
FT	DOMAIN	1374	1392	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1393	1412	S5 OF REPEAT IV.
FT	DOMAIN	1413	1481	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1482	1506	S6 OF REPEAT IV.
FT	DOMAIN	1507	2171	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	458	475	BINDING TO THE BETA SUBUNIT (BY
FT	DOMAIN	684	690	POLY-LEU.

Query Match 6.8%; Score 179.5; DB 1; Length 2171;

Best Local Similarity 18.6%; Pred. No. 3.7e-06;

Matches 99; Conservative 86; Mismatches 181; Indels 167; Gaps 19;

QY 46 CSQDGDGDERLTYPONPESLTVLTANNPVMIPAKSKRAYA-----IFETV 100

DB 362 CKRGWGC-FKHGTTNDNFAMLTIVFOCTIMEGWTDVL---YMWQDAMGVELPWPYFVS 417

QY 101 FTVIGSLFMTNLLTAITYSQF-----RGYL----- 125

DB 418 LVIFGSEFVLNLVGLVSGESKERRKAKARGDFOLKREMQGLEEDLKLGLDWTGAEDI 477

QY 126 -----KSLQTS-----LFRRLGTRAAFEYLSMVGEGGA 156

DB 478 DPENDEGKDEKPRMSMPTSETSVNTENAVAGDIEGNCARLAHRISKS-----K 531

QY 157 FPGATRGPGSTSLRCPRASSSSA-----TTTLTWTGTSPP-WOTWCPACSM 203

DB 532 FSRVWRWRNRFCKRCKRAVKNVFWYLVFLVNLTLITASHYHQPMHLEVDQTAH- 590

QY 204 CMMQCCILSVMTS-----SMGFSASSLCTTCWCCSRSLPMACESTCPTPATCLNG 256

```
Db 591 -----KALLALEFTAEMLMKMYSIGLOAFVSLENRPDCFI-----VCGSILETIIYETKV 640
QY 257 SSPLSCWREPMVGLSLMDMTMLNLIVERFLRIPSMKPMAYVASTVLGVQNMRAFG 316
Db 641 MSPLGISVLRVRLRIFKIRYWSNL-----SNLVASLNSVRSIA 682
QY 317 GILVVY---YVFAITGINLFRGVIALPONGSLAPANGSAPCGSFEOLEYMANNPDDFA 373
Db 683 SLILLFLFIIFSLGMOLFSGKF-----NFEDEMOTRRSTFDNFP 723
QY 374 AALVTLMNLVNNW-QVFLDAYRYSRSPMSK-----IYFVLMWLVSIVWNLFLALIL 427
Db 724 QSLITVFQIITGEDMNSVMTDGIMAYGSPFGMLVCITFIIFICGNYILNLVFLALAV 783
QY 428 ENFL-----HKWDPRSHLOPLAGTPEATYQMTVELLFRDILEPGEDEL 471
Db 784 DNLADAESLTSAQKEEERERKKLART--ASPEKKQEVVGKPALEAKEKEKI 834
```

Search completed: October 8, 2002, 10:03:30  
Job time : 31 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:10:16 ; Search time 67 seconds  
(without alignments)  
1252.277 Million cell updates/sec

Title: US-09-918-359-7  
Perfect score: 2634  
Sequence: 1 MSSACWEATGRCRLGGGMV.....PGEDELTERLSQHPMLICR 485

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1180	44.8	371	4 Q9NT82	Q9nt82 homo sapien
2	345	13.1	819	11 Q9NTNS	Q9ntns raltus norv
3	342	13.0	724	10 Q9ZT83	Q9zt83 arabidopsi
4	342	13.0	733	10 Q94KT8	Q94kt8 arabidopsi
5	342	13.0	775	4 Q9ULQ1	Q9ulq1 homo sapien
6	342	13.0	817	11 Q9EJO0	Q9ejoj mus musculu
7	336	12.8	733	10 Q94BT1	Q94bt1 arabidopsi
8	201	7.6	1643	11 Q91WX9	Q91wx9 raltus norv
9	191.5	7.3	2295	11 Q923K6	Q923k6 raltus norv
10	190	7.2	1602	11 Q91W25	Q91w25 mesocricetu
11	189.5	7.2	2125	5 Q96057	Q96057 halocynthia
12	189	7.2	1912	4 Q95226	Q95226 homo sapien
13	189	7.2	1977	4 Q9UHB1	Q9uhb1 homo sapien
14	189	7.2	2224	4 Q9NTZ6	Q9ntz6 homo sapien
15	186.5	7.1	2162	4 Q9NYZ5	Q9nyz5 homo sapien
16	180.5	6.9	1985	11 Q9JIS7	Q9jis7 mus musculu

17	179.5	6.8	1981	11 Q923Z7	Q923z7 raltus norv
18	177.5	6.7	2331	6 Q9TTA4	Q9tta4 bos taurus
19	175.5	6.7	1834	11 Q9EO59	Q9e059 raltus norv
20	174.5	6.6	1688	13 Q57483	Q57483 rana catesb
21	172	6.5	2169	11 Q92305	Q92305 cavia porce
22	171	6.5	2288	11 Q9WDB8	Q9wdb8 raltus norv
23	171	6.5	2295	11 Q9WUT2	Q9wut2 mus musculu
24	170	6.5	1351	11 Q02789	Q02789 mus musculu
25	170	6.5	2435	5 Q9W433	Q9w433 drosophila
26	169.5	6.4	1536	4 Q9NY44	Q9nyy4 homo sapien
27	169.5	6.4	2373	4 Q96R29	Q96r29 homo sapien
28	168.5	6.4	2333	11 Q89089	Q89089 raltus norv
29	168	6.4	751	13 Q90Z28	Q90z28 sternopygus
30	167.5	6.4	1791	4 Q9UHB0	Q9uhe0 homo sapien
31	167.5	6.4	1791	4 Q9U133	Q9u133 homo sapien
32	167.5	6.4	1981	4 Q9NZC8	Q9nzc8 homo sapien
33	167	6.3	1715	5 Q18840	Q18840 caenorhabdi
34	167	6.3	1765	11 Q9R053	Q9r053 mus musculu
35	167	6.3	1837	5 Q967R4	Q967r4 caenorhabdi
36	165	6.3	1518	5 Q963J6	Q963j6 schistosoma
37	164.5	6.2	588	11 Q91ZP5	Q91zpz mus musculu
38	164	6.2	2506	4 Q9NS88	Q9ns88 mus musculu
39	163.5	6.2	1740	5 Q17314	Q17314 cyanea capi
40	163.5	6.2	1956	4 Q9Y5Y9	Q9y5y9 homo sapien
41	163	6.2	2365	11 Q9JRK5	Q9jrk5 mus musculu
42	162.5	6.2	2146	13 Q9PUM3	Q9pum3 gallus galli
43	162.5	6.2	2321	13 Q9PUM4	Q9pum4 gallus galli
44	162	6.2	414	4 Q96P54	Q96p54 homo sapien
45	162	6.2	528	4 Q96P56	Q96p56 homo sapien

## ALIGNMENTS

## RESULT 1

ID	Q9NT82	PRELIMINARY;	PRT;	371 AA.
AC	Q9NT82;			
DT	01-OCT-2000 (TREMblrel. 15, Created)			
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE	HYPOTHEICAL 42.5 KDA PROTEIN (FRAGMENT).			
GN	DKF2P434M0223.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RA	Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;			
RL	Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; ALJ37479; CAB70760.1; -.			
DR	InterPro; IPR000636; Cation_chan_non_lig.			
DR	InterPro; IPR002111; Cat_channel_Trip.			
DR	InterPro; IPR001682; Channel_pore_Ca_Na.			
DR	Pfam; PF00520; ion_trans; 1.			
KM	Hypothetical protein.			
FT	NON_TER			
SO	SEQUENCE			
QY	Query Match	44.8%; Score 1180; DB 4; Length 371;		
	Best Local Similarity	99.6%; Pred. No. 6,4e-93;		
	Matches	222; Conservative	0; Mismatches	1; Indels
			Gaps	0;
QY	263 WRPEWGLSLMDMTRLMLTLVRFRLRTPSMKPAVAVSYVLGVQNMRAFGGLVVY	322		
DB	149 WRPEWGLSLMDMTRLMLTLVRFRLRTPSMKPAVAVSYVLGVQNMRAFGGLVVY	208		
QY	323 YVVFALIGINLFRGYIVLPGNSSLAPANGSPCGSEFQLEWANNFDFPAALVTLWN	382		
DB	209 YVVFALIGINLFRGYIVLPGNSSLAPANGSPCGSEFQLEWANNFDFPAALVTLWN	268		

QY 363 MYNNQVFLDARYRRSGPWSKITYFLMWLVSSVIMVNFLLALLIENFLHKWDPRSHLOP 442  
 Db 269 MYNNQVFLDARYRRSGPWSKITYFLMWLVSSVIMVNFLLALLIENFLHKWDPRSHLOP 328  
 QY 443 LAGTEPATYOMTVELLFRDILEEPDELETERLSOPHMLOR 485  
 Db 329 LAGTEPATYOMTVELLFRDILEEPDELETERLSOPHMLOR 371

## RESULT 2

O9WTN5 PRELIMINARY: PRT: 819 AA.  
 AC O9WTN5.  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE VOLTAGE-GATED CA CHANNEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY.  
 RX MEDLINE=20218667; PubMed=10753632;  
 RA Ishibashi K., Suzuki M., Imai M.;  
 RT "Molecular cloning of a novel form (two-repeat) protein related to  
 RT voltage-gated sodium and calcium channels.";  
 RT Biochem. Biophys. Res. Commun. 270:370-376(2000).  
 DR EMBL: AB018253; BAA76556.1; -.  
 DR InterPro: IPR000636; Cation\_chan\_non\_1lg.  
 DR InterPro: IPR002111; Cat\_channel\_trpl.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans\_2.  
 DR PROSITE: PS00307; LECTIN LEGUME BETA; UNKNOWN.1.  
 SQ SEQUENCE 819 AA; 94609 MW; A9D3ABAC37BF9E3 CRC64;

Query Match 13.1%; Score 345; DB 11; Length 819;  
 Best Local Similarity 25.7%; Pred. No. 4.5e-21;  
 Matches 117; Conservative 71; Mismatches 164; Indels 104; Gaps 18;

QY 60 YFQNPESLTLVLTITANNPDVMIIPAYSKNRAIAIFPIVTVIGSLFLMNLIAIYS 119  
 Db 263 YFNTLNSIVNLTFLITANPEPDMPSISRNPMSCVEFIYVLSIELYFIMMLIAVVD 322  
 QY 120 QFRGIAMSLQSLFRRLGTRAFEVLSMVGEGAF-----POATRRGPST 167  
 Db 323 TFNDLEKHFKSLHAKRTAIOHAHYLVQSRRPAGISYRQEGIMRFYKPKMSARE--- 379  
 QY 168 SLRCPADSSSSATTTLT-----WGTSFQWTW---CPFACSWCMQMOC 210  
 Db 380 --RFTLFRALNQSNTPPLSLKDFYIEVALQWAKKRNQHPDELPTAFILFKG--- 434  
 QY 211 LLSVTSNGSFSTASLCTT---CW-----SCCSRSLPMACBCTCTPATCLT- 255  
 Db 435 -INILVNSKAIQYFMYLVAVANGVILVETMLKGNLSIKHVPWSY-----LVFLTI 486  
 QY 256 -----GSSPL-----SCWRP-----EMVGLSLMDMTMLNK-----LIVR- 287  
 Db 487 YGVELFMKVVAGIPVEYLSGGMNLFDFSLTAFAGLLAL-----TINNEPFIYVLRP 541  
 QY 288 --FLRIISMKPMVAVSTVGLVONMRAFGSILVVVVYVEAIIIGINLFRGVI---VALP 342  
 Db 542 LQALFLFLKRYKRYNVLDTMELFLPRMASLGLTLTFYSAIVGMEFFSGRLSPNCSTP 601  
 QY 343 GNSSLAPANGS-APCGSEQL-----EYMANNPDDFAALVLTMLNLMVNNQVFLDAARR 397  
 Db 602 ARWGILTPIDSSITRLGNKTKGRKGYLYLNNDNLINSFVTLFELTVANNMIIIMEGVS 661  
 QY 398 YSGPWSKITYFLMWLVSSVIMVNFLLALLIENFLHK 433  
 Db 662 QTSKHSRLYFMETVYLVTVV--MTIIVAILLEAFVR 696

## RESULT 3

O9ZT83 PRELIMINARY: PRT: 724 AA.  
 AC O9ZT83.  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PUTATIVE CALCIUM CHANNEL.  
 GN F9H3.19 OR T5L23.5 OR A74G03560.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Huang E.N., Parnell L.D., de la Bastide M., Schutz K., Habermann K.,  
 RA Dedhia N.N., McComble W.R.;  
 RT "Genomic sequence of Arabidopsis thaliana BAC F9H3, chromosome IV,  
 RT 18.8 cM.";  
 RT Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;  
 RT "BAC F5L23 from chromosome IV, position 19 cM.";  
 RT Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Prestegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,  
 RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,  
 RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W.,  
 RA Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.  
 DR EMBL: AF071527; AAD15312.1; -.  
 DR EMBL: AC005142; AAD15312.1; -.  
 DR EMBL: AL161497; CAB77841.1; -.  
 DR InterPro: IPR000636; Cation\_chan\_non\_1lg.  
 DR InterPro: IPR002111; Cat\_channel\_trpl.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR InterPro: IPR002048; EF-hand.  
 DR InterPro: IPR003015; HLH\_Myc.  
 DR InterPro: IPR001696; Na\_channel.  
 DR Pfam: PF00036; ehand; 2.  
 DR Pfam: PF00520; Ion\_trans; 2.  
 DR PRINTS: PR00170; NACHANNEL.  
 DR SMART: SM00054; EFh; 2.  
 DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN.1.  
 KW Calcium-binding.  
 SQ SEQUENCE 724 AA; 83856 MW; EBA3A27EB15BEF32 CRC64;

Query Match 13.0%; Score 342; DB 10; Length 724;  
 Best Local Similarity 24.1%; Pred. No. 7e-21;  
 Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;

QY 55 RERLTYFQNPESLTLVLTITANNPDVMIIPAYSKNRAIAIFPIVTVIGSLFLMNLIT 114  
 Db 233 QOGLTVFTSYGATLYQMFLLFTTSNNPDVMIIPAYKSSRWSSVFVLYVLIGVYFTNITL 292  
 QY 115 AIYISQFQGLYLMKSLQ-LSLPRRLGTR-----AFEVLS----- 149



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Db 293 AAYYDSFEKDLAKQVSGMDQKRRMLERKAFGLIDSDKNGEIDKNOQIKLFEQOLNRYRLP 352
QY 150 --MWGECA-----PPQATRGST 167
Db 353 KISKEEGLFDELDTDRKINKDEFADLCQALALRFOREVPSLEHFPQIHSALSQ 412
QY 168 SLR-FCRAPSSSA-----TTTLTWGTS--PMQTMCPACSMCW-MQMC 209
Db 413 QLRFAVSPNFGYALISFLINFIYAVVETLIDEESSAKPMQV-AEFGVGMIVYLEMA 471
QY 210 CLLSVMT-----SSW--GFSTASSLCTTCWSCCSRLPACGTCPTPATCLTGSSPLSCW 263
Db 472 --LKITYGFEENYRREGANRFDELVT-----WVL--VIGETATFT----- 508
QY 264 RPEMVGSLTMDTQMLNMLIVFRFLRIPSMKPMNAVASTVLGVMNAFGSILVYV 323
Db 509 -PBNPFSSGEMIRYLLARMLRLILMNVOYRAFIATFTLLPILSLMPTGTEICVL 567
QY 324 YVFAIIGINLFRGVIALPQNSSLAPANGSAPGSGFE---OLEYMANPFDFPAALVTL 379
Db 568 CIYCSIGVOYFGGLVNA--GNKKL-----FETELADDDYLLFNNDYRNGAVTL 614
QY 380 WNLAVVNNVOVFLDAYRRYSGPMSKI-YEVLMLVSSVIYVWNLFLALILENLEHKWD 435
Db 615 FNLLVGNMVOVMESYKDLGTWMSITYEVSFYVITILLNLNLVAVFALEAFTELD 671

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RESULT 4
Q94K18 PRELIMINARY: PRT: 733 AA.
AC 094K18:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE CALCIUM CHANNEL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Fischer M., Knight H., Amtmann A., Sanders D.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF360372; AAK39534.1;
SQ SEQUENCE 733 AA; 84873 MW; 1CA978DB68BFF445 CRC64;

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Query Match 13.0%; Score 342; DB 10; Length 733;
Best Local Similarity 24.1%; Pred. No. 7.1e-21;
Matches 115; Conservative 84; Mismatches 144; Indels 134; Gaps 19;

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QY 55 RERLTFPQNLPESTLSLVLTANNPDVMIIPAYSKNRAVAIFFIYFVIGSLFLEMLLT 114
Db 242 QOGLTFVTSYGATLYQMFLLFTSNPDVMIIPAYSKSRMSVFEVLVYVILGYFVNLTL 301
QY 115 AIYISQFGLYMKSLQ-TSLFRRLRGLTRA-----AFEVLS----- 149
Db 302 AAVYISFEKQLAKQVSGMDQKRRMLERKAFGLIDSDKNGEIDKNOQIKLFEQOLNRYRLP 361
QY 150 --MWGECA-----FPQATRGST 167
Db 362 KISKEEGLFDELDTDRKINKDEFADLCQALALRFOREVPSLEHFPQIHSALSQ 421
QY 168 SLR-FCRAPSSSA-----TTTLTWGTS--PMQTMCPACSMCW-MQMC 209
Db 422 QLRFAVSPNFGYALISFLINFIYAVVETLIDEESSAKPMQV-AEFGVGMIVYLEMA 480
QY 210 CLLSVMT-----SSW--GFSTASSLCTTCWSCCSRLPACGTCPTPATCLTGSSPLSCW 263
Db 481 --LKITYGFEENYRREGANRFDELVT-----WVL--VIGETATFT----- 517
QY 264 RPEMVGSLTMDTQMLNMLIVFRFLRIPSMKPMNAVASTVLGVMNAFGSILVYV 323

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Db 518 -PDENTFFSNGEMIRYLLARMLRLILMNVOYRAFIATFTLLPILSLMPTGTEICVL 576
QY 324 YVFAIIGINLFRGVIALPQNSSLAPANGSAPGSGFE---OLEYMANPFDFPAALVTL 379
Db 577 CIYCSIGVOYFGGLVNA--GNKKL-----FETELADDDYLLFNNDYRNGAVTL 623
QY 380 WNLAVVNNVOVFLDAYRRYSGPMSKI-YEVLMLVSSVIYVWNLFLALILENLEHKWD 435
Db 624 FNLLVGNMVOVMESYKDLGTWMSITYEVSFYVITILLNLNLVAVFALEAFTELD 680

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RESULT 5
Q9ULQ1 PRELIMINARY: PRT: 775 AA.
AC 09ULQ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE KIAA1169 PROTEIN (FRAGMENT).
GN KIAA1169.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL: AB032935; BAA86483.1;
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR002111; Cat_channel_TrypL.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001220; Lectin_legB.
DR InterPro: IPR001696; Na_channel.
DR Pfam: PF00520; ion_trans_2.
DR PRINTS: PR00170; NACHANNEL.
DR PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 775 AA; 90039 MW; 7084CC9A7F62E85 CRC64;

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Query Match 13.0%; Score 342; DB 4; Length 775;
Best Local Similarity 25.4%; Pred. No. 7.6e-21;
Matches 117; Conservative 71; Mismatches 158; Indels 114; Gaps 17;

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QY 60 YFONLPESTLSLVLTANNPDVMIIPAYSKNRAVAIFFIYFVIGSLFLEMLLT 119
Db 221 YESTLENSIVSLFVLLTANNPDVMIIPAYSKSRMSVFEVLVYVILGYFVNLTL 280
QY 120 QRGYIMKSLQTSLEFRRLGLTRAFAEVLSSMWGECAFPQATRGSTSLRCRAPSSSS 179
Db 281 TENDIEKKRKFSLMLKRTAIOHAYRLISORRPAG---ISYRQPEGLMRFYK-PRMSA 335
QY 180 ATTTTL-----TWGSSPQWQTMCPACSMQWQKCLL- 212
Db 336 RERYLTFKALNNQNPFLSLKDFYDIYEVAALAKWKAKKREHW-----FDELPTALLI 389
QY 213 ----SVMTSSWGFSTASSLCTT--CW-----SCCSRLPACGTCPTPATCL 254
Db 390 FGININILVSKAFQYFMYLVAVNGVWILVETFMKLGNFSGHWMS-----LVFL 442
QY 255 T-----GSSPL-----SCWRP-----EAVGLSLTMDTQMLNML- 266
Db 443 TIYGVLEFLKAVAGLGVYELSSGMNLFDSVTVAFLGLAL-----ALNMPFFYIVVL 497
QY 287 R----FLRIPSMKPMNAVASTVLGVMNAFGSILVYVYFAIIGINLFRGVIALP 343
Db 498 RPLQGLRLFKLKERIRNVLDITFELLPRASISGLTLLITFYISFAIYGMFEFGIYFPNCC 557

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;  
 RX MEDLINE=21380268; PubMed=11487617;  
 RA Xu W., Lipscombe D.;  
 RT "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively  
 RT hyperpolarized membrane potentials and are incompletely inhibited by  
 RT dihydropyridines."  
 RL J. Neurosci. 21:5944-5951(2001).  
 DR EMBL: AF370009; AAK72959.1;  
 SQ SEQUENCE 1643 AA; 186828 MW; 97AA34B073EA520 CRC64;

Query Match 7.6%; Score 201; DB 11; Length 1643;  
 Best Local Similarity 18.2%; Pred. No. 2, 1e-08;  
 Matches 93; Conservative 82; Mismatches 174; Indels 162; Gaps 17;

OY 12 CRGGGMVPTGVGRGLESLMGDDPVVWMSRCFSQODDQDRERLTYPONLEPSLSTL 71  
 Db 324 CR--SGVGVPGGI-----TTFDNPFAMLTV 348  
 OY 72 LVLTITANPDVMIYASKNRAYA-----IFETVYIGSLFNLNLTATITISQFRTLM 126  
 Db 349 FQGITMGMTDVL---YVWDALGEMWVYEVSLITGSEFVNLVLGLSGF----- 400  
 OY 127 KSIQTSIFRRRLGTRAFFVLS-----MVGEGAFPOATRGPSTSLRFC 172  
 Db 401 -----SKERKAKARGFQKLRKQLEEDLKGILDMITQAEIDIDPENEGGEGKRN 455  
 OY 173 RAPSSSATTTLTWGTSSPMOTWCPFACSMQMCCLLSVMTSS---WGFSTASSLCT 229  
 Db 456 SMTST--TTSVNTENVSGGEGTGCCGSLMCMWRKRAAKTGPSCGRGMAISKSL 513  
 OY 230 TCWSSCSRLPMACEGTCTPA-----TCLTGSSP----- 259  
 Db 514 RRRRRNRNRRRRRAAVKSVTFYWLIVLVNLTILISEHNQDPWLQIODIANKYL 573  
 OY 260 LSCWREP-----VGLLSIMD-----TRMLNMLTV-----FR 287  
 Db 574 LALFTEMLVKMTSLGIQAVFSLFRFDCFVVCGGITETILVELLSPLGVSFRCVR 633  
 OY 288 FLRIIPSMKPMAYASTVLGIYONMRAFGIIVVY---YVFALIGNLFRTGYVALPGN 344  
 Db 634 LRIFVYTRHMTSLNVLVASLMSKSIASLILFLFTITISLGMQLEGKRF----- 687  
 OY 345 SSILAPNGSAPGSGEQLEYMANNFDAALVTLMNVVNWQ--VFLDAYRRYSQPM 403  
 Db 688 -----NFEDETQTKRSTFENFPQALLTFQILGEDMNVAMVDGIMAYGPPS 734  
 OY 404 K-----YFVLMWLVSVIWNLFALILEN 429  
 Db 735 SGMIVCIYIIIFIGCNITLLNVLAIADVN 765

## RESULT 9

O923K6

AC 0923K6; PRELIMINARY; PRT; 2295 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CALCIUM CHANNEL ISOFORM ALPHA17.  
 GN CAV2.3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Mitchell J.W., Larsen J.K., Best P.M.;  
 RT "Identification of the Calcium Channel alpha1e (Ca2.3) Isoform

RT Expressed in Atrial Myocytes."  
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY029412; AAK33009.1;  
 SQ SEQUENCE 2295 AA; 259227 MW; 7AE2D2DEC30E64F CRC64;

Query Match 7.3%; Score 191.5; DB 11; Length 2295;  
 Best Local Similarity 22.2%; Pred. No. 2e-07;  
 Matches 105; Conservative 79; Mismatches 187; Indels 103; Gaps 20;

OY 32 LMGGPVVWMSRCFSQODDQD-----RERLTYPONLEPSLSTLVLITANPNVMPA 87  
 Db 259 LEGPDPHPPCGVQCGPAGYECKDWIGPDGTFQDFNLPAVLTVRQGITMGMTVL--- 315  
 OY 88 YSKNRAYA-----IFETVYIGSLFNLNLTATITISQF-----RGYIMSLQTS 132  
 Db 316 YNTNDALGATWNLVYFIPLIITGSEFVNLVLGLSGFAERERENRRAPFKLRQO 375  
 OY 133 LFRRRLGTRA-----AFEVL---SMVGECAFPOATRGPSTSLR--FCRAPSSSATTTL 184  
 Db 376 IERELNGTRAWIDKAEVYMLAEKNKSGTSALEVRATIRKSRTEAMTRDSSDEHCYDI 435  
 OY 185 TTWGT---SSPMOTWCPFACSMQMCCLLSV--MTSS---WGFSTASSLCTTQMSC 234  
 Db 436 SSVGTPLARASIKSTKVDGASYFRHKERLKRISIRHWKSGVFYIYLVVALNTACVAT 495  
 OY 235 CSRSLP-WACE-----GTCPPTATCLGSSPLSCWR--PENYGL 270  
 Db 496 VHNQPPQMLHLLYAEFLGLFLDMSLKMVGMPR---LYHSSFNCFDEGVTVGS 551  
 OY 271 L--SLMDTRM-----LNLIVFRRLRIPSKPMAYASTVLGIYONMRAFGIIVVY 323  
 Db 552 IFEVYMAIFPRGTGFGSLVALRLRLRITKTKYASIRNLVYLSMSKSIISLTLFLF 611  
 OY 324 ---YVFALIGNLFRTGYVALPGNSILAPANGSAPGSGEQLEYMANNFDAALVTLM 380  
 Db 612 LFTVFEALLMQLEFGFRFNNDGTPSA-----NDFEPAAIMTVF 651  
 OY 381 NLMVNNM--QVFLDAYRRY---SGPMSKIYFVLMWLVSVIWNLFALILEN 429  
 Db 652 QILGEDMNEVLNGLIRSGGSSGMSAIFYTLFGNITLLNVLAIADVN 705

## RESULT 10

O91W25

AC 091W25; PRELIMINARY; PRT; 1602 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA1 SUBUNIT.  
 GN CAV1.3 (ALPHA1D).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HIT CELL;  
 RX MEDLINE=21329586; PubMed=11435619;  
 RA Schnitz A., Plant T.D., Dolphin A.C., Nuenberg B.;  
 RT "Functional expression and characterization of a voltage-gated Cav1.3  
 RT (alpha1d) calcium channel subunit from an insulin-secreting cell  
 RT line."  
 RL Mol. Endocrinol. 15:1211-1221(2001).  
 DR EMBL: AJ311617; CAC48390.1;  
 SQ SEQUENCE 1602 AA; 181297 MW; 4207378974DE2456 CRC64;

Query Match 7.2%; Score 190; DB 11; Length 1602;  
 Best Local Similarity 17.9%; Pred. No. 1.8e-07;  
 Matches 91; Conservative 87; Mismatches 173; Indels 158; Gaps 18;

OY 6 WEATGR-CRLGG-----GMVPTGVGRGLESLMGDDPVVWMSRCFSQODDQDQDRERLT 59

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Db      310  FSGNGRQCAVNGEBCRSGWGPNGI-----T 336
Qy      60  YFQMLPESTLSLVLTLLTANNPDVMIIPAYSKNAYA----IFFYFVIGSLFELMLNLT 114
Db      337  NFDNFAPFAMLTVFCGCIIMEGWTDLV---YMNNDAMGFELEPMVYFSLVIFGSEFYLNLTVL 393
Qy      115  AITYSQREGIYMLKSLQTSILRRRLIGTAAAEVYLSMWG-----EGGAFPOA 160
Db      394  GVLGGEFSKEREKARKAGDQKLEKQOULEDLKGYLDWTQOEDIDPENEEGGEGRK 453
Qy      161  TRRGPSLIRRCRAPSSSSATITTLTWGT-----SSPWQTCPF-----A 200
Db      454  NTSMPSTESTSVNTEENNSGEEHOGSGSLQAIKSKLSRRMRNRMRFRRCRAAVKS 513
Qy      201  GSWCMQMOCCI-LSVMYSS-----WGF-----STASSLCTTWCSC-----CSRSLP- 240
Db      514  VTFYWLIVLVEFLMTLITSEHYNQDPMLQIOIDIANKVLLAFETCMLVKNMSTLSQAY 573
Qy      241  -----WAGEGCPPTATCOTSSPSCWRPMWGLSLMDTRMLNMLIYERFL 289
Db      574  FVSLFNRPDCVYVCGGITETLIVLELMSLPAG-----VSVFRCVRL 615
Qy      290  RIIPSMKPMAYAVASTVLGLVONMRAFGGILVYVY---YFAIGINLFRGIVYALPENGSS 346
Db      616  RIFKXTRMTLSLNNVYASLNSMSIASLTLLEFLIFIIISLGMOLFGRKF----- 667
Qy      347  IAPANGSAPCGSEFOLEKWMANNFDDFAALVLTMLNMLVNNMQ-VFLDAYRRYSGPMSK- 404
Db      668  -----NFDQTKRSTFDFNFDPALLTFVQILTGEDMNAVMYDGMAYGGPSSSG 716
Qy      405  -----IYFVLMVLSSYIVWNLFLAIIEN 429
Db      717  MIVCIYFIITFCGNYILNLFALIAVUN 745

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RESULT 11
096057 ID 096057 PRELIMINARY; PRT; 2125 AA.
AC 096057;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ASCIDIAN CALCIUM CHANNEL ALPHA1-SUBUNIT.
GN TUCAL1.
OS Halocynthia roretzi (sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamura Y., Okagaki R.;
RT "Tucal, ascidian calcium channel alpha1-subunit.";
RL Submitted (MAY-1998) to the EMBL/Genbank/DDBJ databases.
DR EMBL: AB013604; BAA34927.2;
DR InterPro: IPR000636; Cation_chan_non_1lg.
DR InterPro: IPR002111; Cat_channel_Tryp.
DR InterPro: IPR002077; Ca_channel.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR001696; Na_channel.
DR Pfam: PF00520; Ion_trans_4.
DR PRINTS: PR00167; CACHANNEL.
DR PRINTS: PR00170; NACHANNEL.
SQ SEQUENCE 2125 AA; 242981 MW; 7CBB25B37A10FC0 CRC64;

Query Match 7.2%; Score 189.5; DB 5; Length 2125;
Best Local Similarity 20.2%; Pred. NO. 2.7e-07;
Matches 99; Conservative 76; Mismatches 159; Indels 157; Gaps 20.

33 WGGDVVVRWKSRCFGS-----QDDDGQDGRRLYFQNLPESLSLYLTANNPPVMIPA 87
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
234 WC-----RHSGGGMICESDMAGPSKGIINFDTFYAIVTVQCITMGMTDYL---- 281
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[illegible]

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RESULT 12
0955226 PRELIMINARY; PRT; 1912 AA.

ID 095226 AC 095226;
DT 01-MAY-1999 (TREMblrel, 10, Created)
DT 01-MAY-1999 (TREMblrel, 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, Last annotation update)
DE VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.
GN CACNA1F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bech-Hansen N.T., Naylor M.J., Maybaum T.A., Pearce W.G., Koop B.,
RA Fishman G.A., Mets M., Musarella M.A., Boycott K.M.;
RT "Loss-of-function mutations in a novel retinal gene in Xp11.23 cause
RT incomplete CSNB.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067227; AAD03587.1; -
DR InterPro: IPR000636; Cation_chan_non_119.
DR InterPro: IPR002111; Cat_channel_Tryp.
DR InterPro: IPR002077; Ca_channel.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR Pfam: PF00520; Ion_Trans; 4.
DR PRINTS; PR00167; CACHANNEL.
SQ SEQUENCE 1912 AA; 214031 MW; 0E2C45C8E4156E0D CRC64;

Query Match 7.2%; Score 189; DB 4; Length 1912;
Best Local Similarity 18.3%; Pred. No. 2.7e-07;
Matches 102; Conservative 79; Mismatches 157; Indels 220; Gaps 22;

OY 4 ACWEATGRCRLGGWVPTGTVWVRLGIELSLWGDPPVPMWSCRFCSQDDGQDRERLITYQN 63
DB 226 ACTLNGTECR--GRMPGNGCI-----TNDN 250
OY 64 LDESLTSLVLTITANPNPVMIPAYSKNRAY-----IFEIFYIGSLFNLMLTALY 118
DB 251 FFEMATLPPQCTMGEGTIVL--TWMDAMGIELEPWTFTSVLYIFGSEFVNLVIGVYS 307

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QY 119 SOF-----RGYLMKSLOTSLFRRRLGTRAAFEVLSSWVG 152  
 Db 308 GEFSEREKAKARGDFOKOREQOMEEDLRGL--DWITQAEELMEDPESADNIGSMAE 365  
 QY 153 EG--GAPFOAT-----RGPSTSLRF-----CRAPSSSATTTLTWTGSSPWQTM----- 196  
 Db 366 EGRAGHRPOLAEELNRRRG--RLKWFHSHSTRSHSTSHSLPASPDTGSMETGTGDEDE 422  
 QY 197 -----C-----CPACSMC----- 204  
 Db 423 EEGALASCTRCINKIMKTRVCRRLRANRVLARCRBRAVKSACWAVALLVFLNTLTIA 482  
 QY 205 -----WMO-----MCCLISV--MTSSWGFSTASSICT-----TCMSCCSRSLP 240  
 Db 483 SEHNGOPVWLQIOEYANKVLCFTVEMLTKLYGLGPSAYVSFEFNREDFCVGCG----- 538  
 QY 241 WACBGTCTPATCGLGSSPLSCWREPMVGLSLMDTMRMLNMLYFRRLRIIPSKPMAY 300  
 Db 539 -----GILETTIVEGAMQPLG-----ISVLRVRLRLRIKVTIRHMAS 576  
 QY 301 VASTVLGLVQNMRAFGILVVY---YVFAIIGINLFRGVIALPONGSLAPANGSAPCG 357  
 Db 577 LSNIVASILNSMKSIASILLFLFIIFSLGMLFGSKF----- 617  
 QY 358 SFEOLEYANNDDPAALVTLMLNMLVNNQVFL--DAYRRYSGWSK-----IYFVLMW 411  
 Db 618 NFDQTHRKSTFEDTPOALLTVFOILTGEDMNVVMDGIMAYGPFPGMLVCIFYILLF 677  
 QY 412 LVSSVIVNLFALILEN 429  
 Db 678 ICGNTIILNVLALAVDN 695

## RESULT 13

09UHB1

ID 09UHB1 PRELIMINARY: PRT: 1977 AA.

AC 09UHB1;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 13, Last annotation update)  
 DE VOLTAGE-GATED L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20334628; PubMed=10873387;  
 RA Naylor M.J., Rancourt D.E., Bech-Hansen N.T.;  
 RT "Isolation and Characterization of a Calcium Channel Gene, Cacna1f,  
 the Murine Orthologue of the Gene for Incomplete X-Linked Congenital  
 RT Stationary Night Blindness."  
 RL Genomics 66:324-327(2000).  
 DR EMBL: AF201304; AAF15290.1;  
 DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
 DR InterPro: IPR002111; Cat\_channel\_TPrL.  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR InterPro: IPR001696; Na\_channel.  
 DR Pfam: PF00520; Ion\_trans\_4.  
 DR PRINTS: PR00167; CACHANNEL.  
 DR PRINTS: PR00167; CACHANNEL.  
 DR PRINTS: PR00167; CACHANNEL.  
 SQ SEQUENCE 1977 AA; 220676 MW; 35433650C6DBE73 CRC64;

Query Match 7.2%; Score 189; DB 4; Length 1977;

Best local Similarity 18.3%; Pred. No. 2.8e-07; Mismatches 157; Indels 220; Gaps 22;

QY 4 ACWEATGRCLRGGMVPTGVNRGLSLWGGDPVWPCSRFCSQODGDGDRERLTYPON 63  
 Db 291 ACTLNGTECR--GRMPGPNGI-----TNDN 315

QY 64 IPESLTSLLVLTITANPDVIMIPAYSKNRVA-----IFFVETVIGSLFLNLTITALLY 118  
 Db 316 PEFAMLTVPQCTMGMTDVL---YMODAMGYELPMWYFVSLVIFGSEFVNLVIGVLS 372  
 QY 119 SOF-----RGYLMKSLOTSLFRRRLGTRAAFEVLSSWVG 152  
 Db 373 GEFSEREKAKARGDFOKOREQOMEEDLRGL--DWITQAEELMEDPESADNIGSMAE 430  
 QY 153 EG--GAPFOAT-----RGPSTSLRF-----CRAPSSSATTTLTWTGSSPWQTM----- 196  
 Db 431 EGRAGHRPOLAEELNRRRG--RLKWFHSHSTRSHSTSHSLPASPDTGSMETGTGDEDE 487  
 QY 197 -----C-----CPACSMC----- 204  
 Db 488 EEGALASCTRCINKIMKTRVCRRLRANRVLARCRBRAVKSACWAVALLVFLNTLTIA 547  
 QY 205 -----WMO-----MCCLISV--MTSSWGFSTASSICT-----TCMSCCSRSLP 240  
 Db 548 SEHNGOPVWLQIOEYANKVLCFTVEMLTKLYGLGPSAYVSFEFNREDFCVGCG----- 603  
 QY 241 WACBGTCTPATCGLGSSPLSCWREPMVGLSLMDTMRMLNMLYFRRLRIIPSKPMAY 300  
 Db 604 -----GILETTIVEGAMQPLG-----ISVLRVRLRLRIKVTIRHMAS 641  
 QY 301 VASTVLGLVQNMRAFGILVVY---YVFAIIGINLFRGVIALPONGSLAPANGSAPCG 357  
 Db 642 LSNIVASILNSMKSIASILLFLFIIFSLGMLFGSKF----- 682  
 QY 358 SFEOLEYANNDDPAALVTLMLNMLVNNQVFL--DAYRRYSGWSK-----IYFVLMW 411  
 Db 683 NFDQTHRKSTFEDTPOALLTVFOILTGEDMNVVMDGIMAYGPFPGMLVCIFYILLF 742  
 QY 412 LVSSVIVNLFALILEN 429  
 Db 743 ICGNTIILNVLALAVDN 760

## RESULT 14

09NYZ6

ID 09NYZ6 PRELIMINARY: PRT: 2224 AA.

AC 09NYZ6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CALCIUM CHANNEL ALPHA1E SUBUNIT, DELTA39 SPLICED VARIANT  
 DE (FRAGMENT).  
 GN CACNA1E.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Miltman S., Agnew W.S., Malek J.A.;  
 RT "Exon Organization and Alternative Splicing of CACNA1E."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF233391; AAF37687.1;  
 DR EMBL: AF239258; AAF37687.1; JOINED.  
 DR EMBL: AF239259; AAF37687.1; JOINED.  
 DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
 DR InterPro: IPR002111; Cat\_channel\_TPrL.  
 DR InterPro: IPR002077; Ca\_channel.  
 DR InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 DR Pfam: PF00520; Ion\_trans\_4.  
 DR PRINTS: PR00167; CACHANNEL.  
 DR PRINTS: PR00167; CACHANNEL.  
 FT NONTER 1  
 SQ SEQUENCE 2224 AA; 251889 MW; 67D34234924F6690 CRC64;

Query Match 7.2%; Score 189; DB 4; Length 2224;

Best local Similarity 19.4%; Pred. No. 3.2e-07; Mismatches 218; Indels 132; Gaps 20;

QY 32 LMGDPVWPCSRFCSQODGDGOD---RERLTYPONIPESLTSLLVLTITANPDVIMIPA 87

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Db 170 LGGFDPHPCGVGCGPAGYECKDWIGPNDGITOFPDNLFAVLTVFQCITMEGTVL--- 226
QY 88 YSKNRAYA-----IFFIVTVIGSLFLMNLTAIYSQF-----RGYLMKSLQTS 132
Db 227 YNTNDALGATWMLYFIPLIIIGSFVNLVLGVLGSEFAKEREVENRRAFMKLRQOQ 286
QY 133 LFRRLGTAAFEVLSMWEGGAFPOATRGPSTSLRCPARSSSSATTTLTWTGSSP 192
Db 287 IERELNGYRAWIDKAEVW-----LAENKNAGTSALEVLRATIKRSTTEAMTRDSSDE 341
QY 193 W-----QWCPFACS-----WCWMQMCCLLSV--MTSS---WGFSTASLCT 229
Db 342 HCVDISSVGTPLARASIKSAKVDGVSFYFRKRELRLRISIRHMVKSQVFWYIVLSVALNT 401
QY 230 TCWSCCSRSLP-WACE-----GTCPPATVCLTGSSPLSCMR-P 265
Db 402 ACVAIVHNNQPOWLTLLYYAEFLGLFLLEMSLKMVGMPR---LYFHSSEFCDFG 457
QY 266 EMVGLL--SLMDMTRM-----LNLIVFRRLIIPSMKPMAYVASTVLGVONMRAFGGI 318
Db 458 VVGSIFEVVAIFRPGTSEGISVLRALRLRIKTKYWSLRLNVLVSLMSSMKSIISL 517
QY 319 LVVVY---YVFAIGINLFRGVIALPGNSSLAPANGSAPCGSPOLEYANNEDFPAA 375
Db 518 LFLFLFIVFVALLGMQLFGFRFNFNDGTPSA-----NEDFPAA 557
QY 376 LVTLMLNMLVNNM--OVFLDAYRY---SGPWSKIYFVLMWLVSSVYVWVLFALLIENF 430
Db 558 IMTFVQILTGEDMNEVMYNGIRSGGVSGWMSAIFYIVLILFGNTLLNVFLAIVADNL 617
QY 431 L-----HKWDPRSILOPLAGTPEATYQMTVELLFEDLIEEGEDEL 471
Db 618 ANAQELTKDQEEEAFAFNKHALQKAKEVSPMSAPRMPSTIEDRRRRHMSMWEDRSSHL 677
QY 472 TERLSQH 478
Db 678 RERRRRH 684

RESULT 15
Q9NYZ5 PRELIMINARY; PRT; 2162 AA.
AC Q9NYZ5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE CALCIUM CHANNEL ALPHAIE SUBUNIT, DELTA19 DELTA46 SPLICED
DE VARIANT (FRAGMENT).
GN CACNAIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miltman S., Agnew W.S., Malek J.A.;
RT "Exon Organization and Alternative Splicing of CACNAIE.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF223391; AAF37688.1;
DR EMBL; AF239238; AAF37688.1; JOINED.
DR EMBL; AF239259; AAF37688.1; JOINED.
DR InterPro; IPR000636; Cation_chan_non_1ig.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
FT NON_TER 1
SQ SEQUENCE 2162 AA; 244728 MW; 9D40173993B9E261 CRC64;

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Query Match 7.1%; Score 186.5; DB 4; Length 2162;  
Best Local Similarity 20.5%; Pred. No. 5.1e-07;

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Matches 98; Conservative 84; Mismatches 184; Indels 113; Gaps 19;
QY 32 LMGGDPVPMSCRFCSQODGOD---RERUTYFQNLPESTLSLVLTTANNPDVWIPA 87
Db 170 LGGFDPHPCGVGCGPAGYECKDWIGPNDGITOFPDNLFAVLTVFQCITMEGTVL--- 226
QY 88 YSKNRAYA-----IFFIVTVIGSLFLMNLTAIYSQF-----RGYLMKSLQTS 132
Db 227 YNTNDALGATWMLYFIPLIIIGSFVNLVLGVLGSEFAKEREVENRRAFMKLRQOQ 286
QY 133 LFRRLGTAAFEVLSMWEGGAFPOATRGPSTSLRCPARSSSSATTTLTWTGSSP 192
Db 287 IERELNGYRAWIDKAEVW-----LAENKNAGTSALEVLRATIKRSTTEAMTRDSSDE 341
QY 193 W-----QWCPFACS-----WCWMQMCCLLSV--MTSS---WGFSTASLCT 229
Db 342 HCVDISSVGTPLARASIKSAKVDGVSFYFRKRELRLRISIRHMVKSQVFWYIVLSVALNT 401
QY 230 TCWSCCSRSLP-WACE-----GTCPPATVCLTGSSPLSCMR-P 265
Db 402 ACVAIVHNNQPOWLTLLYYAEFLGLFLLEMSLKMVGMPR---LYFHSSEFCDFG 457
QY 266 EMVGLL--SLMDMTRM-----LNLIVFRRLIIPSMKPMAYVASTVLGVONMRAFGGI 318
Db 458 VVGSIFEVVAIFRPGTSEGISVLRALRLRIKTKYWSLRLNVLVSLMSSMKSIISL 517
QY 319 LVVVY---YVFAIGINLFRGVIALPGNSSLAPANGSAPCGSPOLEYANNEDFPAA 375
Db 518 LFLFLFIVFVALLGMQLFGFRFNFNDGTPSA-----NEDFPAA 557
QY 376 LVTLMLNMLVNNM--OVFLDAYRY---SGPWSKIYFVLMWLVSSVYVWVLFALLIENF 429
Db 558 IMTFVQILTGEDMNEVMYNGIRSGGVSGWMSAIFYIVLILFGNTLLNVFLAIVADNL 616

Search completed: October 8, 2002, 10:04:57
Job time : 72 secs

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